STIC-Biotech/ChemLib 119643

From: Hamud, Fozia
Sent: Sunday, April 18, 2004 8:10 AM
To: STIC-Biotech/ChemLib
Subject: sequence search for 09/989725

Kindly search SEQ ID NO:417 of 09/989725 against commercial and interference data bases. Thanks.

Fozia Hamud
Patent Examiner
Art Unit 1647
Remsen: Room 4D64
Mail Box Remsen: 4C70
272-0884

Searcher:_____
Phone:_____
Location:_____
Date Picked Up: 4/20/04
Date Completed: 4/20/04
Searcher Prep/Review:_____
Clerical:_____
Online time:_____

TYPE OF SEARCH: /
NA Sequences:_____
AA Sequences:_____
Structures:_____
Bibliographic:_____
Litigation:_____
Full text:_____
Patent Family:_____
Other:_____

VENDOR/COST (where applic.)
STN:_____
DIALOG:_____
Questel/Orbit:_____
DRLink:_____
Lexis/Nexis:_____
Sequence Sys.: 004
WWW/Internet:_____
Other (specify):_____

STIC Search Report
Biotech-Chem Library

STIC Database Tracking Number: 119643

TO: Fozia Hamud **Location: REM/4D64/4C70** **Art Unit: 1647** **Tuesday, April 20, 2004** **Case Serial Number: 09/989725**	**From: Edward Hart** **Location: Biotech-Chem Library** **REM-1A55** **Phone: 571-272-2512** **edward.hart@uspto.gov**

Search Notes

Examiner Hamud,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Edward Hart

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 20, 2004, 01:40:55 ; Search time 692 Seconds
(without alignments)
10608.217 Million cell updates/sec

Title: US-09-989-725-417
Perfect score: 1728
Sequence: 1 cagccgggtcccaagcctgt.....aataatttttgaaacatcaa 1728

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_29Jan04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002s:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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2	1728	100.0	1728	4	AAC91568	Aac91568 Human PRO
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ALIGNMENTS

RESULT 1
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ID AAZ65108 standard; cDNA; 1728 BP.
XX
AC AAZ65108;
XX
DT 05-APR-2000 (first entry)
XX
DE Membrane-bound protein PRO1375 encoding cDNA.
XX
KW Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;
KW pharmaceutical; receptor immunoadhesin; gene mapping; ss.
XX
OS Homo sapiens.
XX
PN WO9963088-A2.
XX
PD 09-DEC-1999.
XX
PF 02-JUN-1999; 99WO-US012252.
XX
PR 02-JUN-1998; 98US-0087607P.
PR 02-JUN-1998; 98US-0087609P.
PR 02-JUN-1998; 98US-0087759P.
PR 03-JUN-1998; 98US-0087827P.
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PR 31-AUG-1998; 98US-0098525P.
PR 16-SEP-1998; 98US-0100634P.
PR 12-JAN-1999; 99US-0115565P.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;
PI Wood WI, Yuan J;
XX
DR WPI; 2000-072883/06.
DR P-PSDB; AAY66762.
XX
PT Membrane-bound proteins and related nucleotide sequences.
XX
PS Claim 2; Fig 299; 822pp; English.
XX
CC The invention provides membrane-bound PRO polypeptides and
CC polynucleotides encoding them. The PRO sequences of the invention were
CC identified based on extracellular domain homology screening. The PRO
CC sequences have homology with proteins including LDL receptors, TIE
CC ligands and various enzymes. The membrane-bound proteins and receptor
CC molecules are useful as pharmaceutical and diagnostic agents. Receptor
CC immunoadhesins, for instance, can be used as therapeutic agents to block
CC receptor-ligand interactions. The membrane-bound proteins can also be
CC employed for screening of potential peptide or small molecule inhibitors
CC of the relevant receptor/ligand interaction. The PRO encoding sequences
CC are useful as hybridization probes, in chromosome and gene mapping and in
CC the generation of antisense RNA and DNA. PRO nucleic acid sequences will
CC also be useful for the preparation of PRO polypeptides, especially by
CC recombinant techniques
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SQ Sequence 1728 BP; 438 A; 360 C; 390 G; 540 T; 0 U; 0 Other;

Query Match 100.0%; Score 1728; DB 3; Length 1728;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1728; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGCCGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCC 60

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Db        121 AGGCCTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTTCCGTGCTGCT 180
Qy        181 GCTGGCGCAGCTGTCAGACGCCGCCAAGAATTTCGAGGATGTCAGATGTAAATGTATCTG 240
Db        181 GCTGGCGCAGCTGTCAGACGCCGCCAAGAATTTCGAGGATGTCAGATGTAAATGTATCTG 240
Qy        241 CCCTCCCTATAAAGAAAATTCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTG 300
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Qy       1261 ATCTGGGTATCTGCTGTGTCTGCACTTCATGGTAAACGGGATCTAAAATGCCTGGTGGCT 1320
Db       1261 ATCTGGGTATCTGCTGTGTCTGCACTTCATGGTAAACGGGATCTAAAATGCCTGGTGGCT 1320
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RESULT 2
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ID AAC91568 standard; cDNA; 1728 BP.
XX
AC AAC91568;
XX
DT 21-MAR-2001 (first entry)
XX
DE Human PRO1375 cDNA.
XX
KW Human; PRO; cytostatic; nootropic; neuroprotective; respiratory general;
KW antiinflammatory; antiangiogenic; immunosuppressive; immunostimulant;
KW PRO agonist; cancer; inflammatory disorder; immunological disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200073348-A2.
XX
PD 07-DEC-2000.
XX
PF 30-MAY-2000; 2000WO-US014941.
XX
PR 02-JUN-1999; 99WO-US012252.
PR 22-JUN-1999; 99US-0140650P.
PR 23-JUN-1999; 99US-0141037P.
PR 20-JUL-1999; 99US-0144758P.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 29-OCT-1999; 99US-0162506P.
PR 30-NOV-1999; 99WO-US028313.

PR 01-DEC-1999; 99WO-US028634.
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PR 09-DEC-1999; 99US-0170262P.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030999.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 02-MAR-2000; 2000WO-US005841.
PR 03-MAR-2000; 2000US-0187202P.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W, Kabakoff RC;
PI Shelton DL, Smith V, Watanabe CK, Wood WI;
XX
DR WPI; 2001-016509/02.
DR P-PSDB; AAB50966.
XX
PT Twenty eight nucleic acids encoding PRO polypeptides which are useful for
PT treating various tumors, e.g. breast cancer, and other inflammatory,
PT angiogenic and immunological disorders.
XX
PS Claim 20; Fig 31; 188pp; English.
XX
CC The present sequence is one of twenty eight nucleic acids encoding PRO
CC polypeptides. The PRO polypeptides and their agonists, including
CC antibodies, peptides, and small molecule agonists, may be used to treat
CC various tumours, e.g., cancers such as breast cancer, ovarian cancer,
CC renal cancer, colorectal cancer, uterine cancer, prostate cancer, lung
CC cancer, bladder cancer, central nervous system cancer, melanoma or
CC leukaemia. They are also useful for treating other disorders such as
CC neuronal, glial, astrocytal, hypothalamic and other glandular,
CC macrophagal, epithelial, stromal and blastocoelic disorders, and
CC inflammatory, angiogenic and immunological disorders
XX
SQ Sequence 1728 BP; 438 A; 360 C; 390 G; 540 T; 0 U; 0 Other;

Query Match 100.0%; Score 1728; DB 4; Length 1728;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1728; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    1 CAGCCGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCC 60
Db    1 CAGCCGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCC 60

Qy   61 GGTCGCGGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCCAGCGATGGCGACCCTGTGGGG 120
Db   61 GGTCGCGGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCCAGCGATGGCGACCCTGTGGGG 120

Qy  121 AGGCCTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTTCCGTGCTGCT 180
Db  121 AGGCCTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTTCCGTGCTGCT 180

Qy  181 GCTGGCGCAGCTGTCAGACGCCGCCAAGAATTTCGAGGATGTCAGATGTAAATGTATCTG 240
Db  181 GCTGGCGCAGCTGTCAGACGCCGCCAAGAATTTCGAGGATGTCAGATGTAAATGTATCTG 240

Qy  241 CCCTCCCTATAAAGAAAATTCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTG 300
Db  241 CCCTCCCTATAAAGAAAATTCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTG 300

Qy  301 TGATTGCCTTCATGTTGTGGAGCCCATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTG 360
Db  301 TGATTGCCTTCATGTTGTGGAGCCCATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTG 360

Qy  361 TCTACGCTGTGAATGCAAATATGAAGAAAGAAGCTCTGTCACAATCAAGGTTACCATTAT 420
Db  361 TCTACGCTGTGAATGCAAATATGAAGAAAGAAGCTCTGTCACAATCAAGGTTACCATTAT 420

Qy  421 AATTTATCTCTCCATTTTGGGCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGA 480
Db  421 AATTTATCTCTCCATTTTGGGCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGA 480

Qy  481 GCCCATACTGAAGAGGCGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATAT 540
Db  481 GCCCATACTGAAGAGGCGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATAT 540

Qy  541 TGGGGATCACCAGCCTTTTGCAAATGCACACGATGTGCTAGCCCGCTCCCGCAGTCGAGC 600
Db  541 TGGGGATCACCAGCCTTTTGCAAATGCACACGATGTGCTAGCCCGCTCCCGCAGTCGAGC 600

Qy  601 CAACGTGCTGAACAAGGTAGAATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCA 660
Db  601 CAACGTGCTGAACAAGGTAGAATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCA 660

Qy  661 GCGAAAGTCTGTCTTTGACCGGCATGTTGTCCTCAGCTAATTGGGAATTGAATTCAAGGT 720
Db  661 GCGAAAGTCTGTCTTTGACCGGCATGTTGTCCTCAGCTAATTGGGAATTGAATTCAAGGT 720

Qy  721 GACTAGAAAGAAACAGGCAGACAACTGGAAAGAACTGACTGGGTTTTGCTGGGTTTCATT 780
Db  721 GACTAGAAAGAAACAGGCAGACAACTGGAAAGAACTGACTGGGTTTTGCTGGGTTTCATT 780

Qy  781 TTAATACCTTGTTGATTTCACCAACTGTTGCTGGAAGATTCAAAACTGGAAGCAAAAACT 840
Db  781 TTAATACCTTGTTGATTTCACCAACTGTTGCTGGAAGATTCAAAACTGGAAGCAAAAACT 840

Qy  841 TGCTTGATTTTTTTTTCTTGTTAACGTAATAATAGAGACATTTTTAAAAGCACACAGCTC 900
Db  841 TGCTTGATTTTTTTTTCTTGTTAACGTAATAATAGAGACATTTTTAAAAGCACACAGCTC 900

Qy  901 AAAGTCAGCCAATAAGTCTTTTCCTATTTGTGACTTTTACTAATAAAAATAAATCTGCCT 960
Db  901 AAAGTCAGCCAATAAGTCTTTTCCTATTTGTGACTTTTACTAATAAAAATAAATCTGCCT 960

Qy  961 GTAAATTATCTTGAAGTCCTTTACCTGGAACAAGCACTCTCTTTTTCACCACATAGTTTT 1020
Db  961 GTAAATTATCTTGAAGTCCTTTACCTGGAACAAGCACTCTCTTTTTCACCACATAGTTTT 1020

Qy 1021 AACTTGACTTTCAAGATAATTTTCAGGGTTTTTGTTGTTGTTGTTTTTTGTTTGTTTGTT 1080
Db 1021 AACTTGACTTTCAAGATAATTTTCAGGGTTTTTGTTGTTGTTGTTTTTTGTTTGTTTGTT 1080

Qy 1081 TTGGTGGGAGAGGGGAGGGATGCCTGGGAAGTGGTTAACAACTTTTTTCAAGTCACTTTA 1140
Db 1081 TTGGTGGGAGAGGGGAGGGATGCCTGGGAAGTGGTTAACAACTTTTTTCAAGTCACTTTA 1140

Qy 1141 CTAAACAAACTTTTGTAAATAGACCTTACCTTCTATTTTCGAGTTTCATTTATATTTTGC 1200
Db 1141 CTAAACAAACTTTTGTAAATAGACCTTACCTTCTATTTTCGAGTTTCATTTATATTTTGC 1200

Qy 1201 AGTGTAGCCAGCCTCATCAAAGAGCTGACTTACTCATTTGACTTTTGCACTGACTGTATT 1260
Db 1201 AGTGTAGCCAGCCTCATCAAAGAGCTGACTTACTCATTTGACTTTTGCACTGACTGTATT 1260

Qy 1261 ATCTGGGTATCTGCTGTGTCTGCACTTCATGGTAAACGGGATCTAAAATGCCTGGTGGCT 1320
Db 1261 ATCTGGGTATCTGCTGTGTCTGCACTTCATGGTAAACGGGATCTAAAATGCCTGGTGGCT 1320

Qy 1321 TTTCACAAAAAGCAGATTTTCTTCATGTACTGTGATGTCTGATGCAATGCATCCTAGAAC 1380
Db 1321 TTTCACAAAAAGCAGATTTTCTTCATGTACTGTGATGTCTGATGCAATGCATCCTAGAAC 1380

Qy 1381 AAACTGGCCATTTGCTAGTTTACTCTAAAGACTAAACATAGTCTTGGTGTGTGTGGTCTT 1440
Db 1381 AAACTGGCCATTTGCTAGTTTACTCTAAAGACTAAACATAGTCTTGGTGTGTGTGGTCTT 1440

Qy 1441 ACTCATCTTCTAGTACCTTTAAGGACAAATCCTAAGGACTTGGACACTTGCAATAAAGAA 1500
Db 1441 ACTCATCTTCTAGTACCTTTAAGGACAAATCCTAAGGACTTGGACACTTGCAATAAAGAA 1500
```

```
Qy       1501 ATTTTATTTTAAACCCAAGCCTCCCTGGATTGATAATATATACACATTTGTCAGCATTTC 1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 ATTTTATTTTAAACCCAAGCCTCCCTGGATTGATAATATATACACATTTGTCAGCATTTC 1560

Qy       1561 CGGTCGTGGTGAGAGGCAGCTGTTTGAGCTCCAATATGTGCAGCTTTGAACTAGGGCTGG 1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 CGGTCGTGGTGAGAGGCAGCTGTTTGAGCTCCAATATGTGCAGCTTTGAACTAGGGCTGG 1620

Qy       1621 GGTTGTGGGTGCCTCTTCTGAAAGGTCTAACCATTATTGGATAACTGGCTTTTTTCTTCC 1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 GGTTGTGGGTGCCTCTTCTGAAAGGTCTAACCATTATTGGATAACTGGCTTTTTTCTTCC 1680

Qy       1681 TATGTCCTCTTTGGAATGTAACAATAAAAATAATTTTTGAAACATCAA 1728
             ||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 TATGTCCTCTTTGGAATGTAACAATAAAAATAATTTTTGAAACATCAA 1728
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RESULT 3
AAF30062
ID AAF30062 standard; cDNA; 1728 BP.
XX
AC AAF30062;
XX
DT 30-APR-2001 (first entry)
XX
DE Human cDNA encoding PRO1375.
XX
KW PRO1375; UNQ712; human; immune disease; autoimmune disease;
KW antirheumatic; antiarthritic; antiinflammatory; antianaemic;
KW immunosuppressive; antithyroid; antidiabetic; neuroprotective;
KW hepatotropic; virucide; dermatological; antipsoriatic; antiasthmatic;
KW antiallergic; immunostimulant; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 104. .700
FT /*tag= a
XX
PN WO200105972-A1.
XX
PD 25-JAN-2001.
XX
PF 15-MAR-2000; 2000WO-US006884.
XX
PR 20-JUL-1999; 99US-0144758P.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Fong S, Goddard A, Godowski PJ;
PI Gurney AL, Hillan KJ, Mark MR, Marsters SA, Pitti RM, Tumas D;
PI Watanabe CK, Wood WI;
XX
DR WPI; 2001-103149/11.
DR P-PSDB; AAB20120.
XX
PT New PRO polypeptides, nucleic acids and (ant)agonists, useful for
PT diagnosing and treating immune-related disorders, such as multiple
PT sclerosis, rheumatoid arthritis and diabetes.
XX
PS Claim 21; Fig 25; 127pp; English.
XX
CC The present sequence is that of cDNA clone DNA67004-1614 (ATCC 203115)
CC encoding novel human immunomodulator protein PRO1375 (UNQ712) (see
CC AAB20120). The clone was isolated from a pancreas cDNA library. PRO1375
CC has a mol.wt. of 22 kDa and a pI of 8.47. The invention provides
CC polynucleotides (see AAF30050-62) encoding novel human PRO proteins (see
CC AAB20108-20) including PRO1375. Claimed compositions comprising these
CC proteins or their agonists are useful for increasing infiltration of
CC inflammatory cells into a tissue of a mammal, stimulating or enhancing an
CC immune response in a mammal, or increasing the proliferation of T-
CC lymphocytes in a mammal in response to an antigen. Claimed compositions
CC comprising the PRO polypeptide or its antagonist have the opposite
CC effect. A claimed method for treating an immune related disorder, such as
CC a T cell disorder, involves administering the PRO polypeptide, an agonist
CC antibody or an antagonist antibody. The disorder is selected from
CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
CC juvenile chronic arthritis, spondyloarthropathy, systemic sclerosis,
CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic
CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
CC thrombocytopaenia, thyroiditis, diabetes mellitus, immune-mediated renal
CC disease, demyelinated diseases (such as multiple sclerosis), autoimmune
CC chronic active hepatitis, primary biliary cirrhosis, granulomatous
CC hepatitis, sclerosing cholangitis, inflammatory bowel disease (ulcerative
CC colitis and Crohn's disease), gluten-sensitive enteropathy, Whipple's
CC disease, (auto)immune-mediated skin diseases (such as bullous skin
CC disease, erythema multiforme and psoriasis), allergic diseases (such as
CC asthma, allergic rhinitis, atopic dermatitis, food hypersensitivity and
CC urticaria), immunologic diseases of the lung and transplantation
CC associated diseases (such as graft rejection and graft-versus-host
CC disease) (all claimed). Claimed methods of diagnosing these disorders
CC comprise detecting the level of expression of the PRO gene. Also claimed
CC are a method of identifying a compound capable of inhibiting the
CC expression or activity of the PRO polypeptide, vectors, host cells,
CC antibodies and a method of stimulating the proliferation of T-lymphocytes
CC using PRO1375
XX
SQ Sequence 1728 BP; 438 A; 360 C; 390 G; 540 T; 0 U; 0 Other;

Query Match 100.0%; Score 1728; DB 4; Length 1728;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1728; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 CAGCCGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CAGCCGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCC 60

Qy         61 GGTCGCGGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCCAGCGATGGCGACCCTGTGGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGTCGCGGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCCAGCGATGGCGACCCTGTGGGG 120

Qy        121 AGGCCTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTTCCGTGCTGCT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AGGCCTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTTCCGTGCTGCT 180

Qy        181 GCTGGCGCAGCTGTCAGACGCCGCCAAGAATTTCGAGGATGTCAGATGTAAATGTATCTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCTGGCGCAGCTGTCAGACGCCGCCAAGAATTTCGAGGATGTCAGATGTAAATGTATCTG 240

Qy        241 CCCTCCCTATAAAGAAAATTCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CCCTCCCTATAAAGAAAATTCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTG 300

Qy        301 TGATTGCCTTCATGTTGTGGAGCCCATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGATTGCCTTCATGTTGTGGAGCCCATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTG 360

Qy        361 TCTACGCTGTGAATGCAAATATGAAGAAAGAAGCTCTGTCACAATCAAGGTTACCATTAT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TCTACGCTGTGAATGCAAATATGAAGAAAGAAGCTCTGTCACAATCAAGGTTACCATTAT 420

Qy        421 AATTTATCTCTCCATTTTGGGCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AATTTATCTCTCCATTTTGGGCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGA 480

Qy        481 GCCCATACTGAAGAGGCGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATAT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GCCCATACTGAAGAGGCGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATAT 540

Qy        541 TGGGGATCACCAGCCTTTTGCAAATGCACACGATGTGCTAGCCCGCTCCCGCAGTCGAGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TGGGGATCACCAGCCTTTTGCAAATGCACACGATGTGCTAGCCCGCTCCCGCAGTCGAGC 600

Qy        601 CAACGTGCTGAACAAGGTAGAATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        601 CAACGTGCTGAACAAGGTAGAATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCA 660

Qy        661 GCGAAAGTCTGTCTTTGACCGGCATGTTGTCCTCAGCTAATTGGGAATTGAATTCAAGGT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GCGAAAGTCTGTCTTTGACCGGCATGTTGTCCTCAGCTAATTGGGAATTGAATTCAAGGT 720

Qy        721 GACTAGAAAGAAACAGGCAGACAACTGGAAAGAACTGACTGGGTTTTGCTGGGTTTCATT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GACTAGAAAGAAACAGGCAGACAACTGGAAAGAACTGACTGGGTTTTGCTGGGTTTCATT 780

Qy        781 TTAATACCTTGTTGATTTCACCAACTGTTGCTGGAAGATTCAAAACTGGAAGCAAAAACT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TTAATACCTTGTTGATTTCACCAACTGTTGCTGGAAGATTCAAAACTGGAAGCAAAAACT 840

Qy        841 TGCTTGATTTTTTTTTTCTTGTTAACGTAATAATAGAGACATTTTTAAAAGCACACAGCTC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TGCTTGATTTTTTTTTTCTTGTTAACGTAATAATAGAGACATTTTTAAAAGCACACAGCTC 900

Qy        901 AAAGTCAGCCAATAAGTCTTTTCCTATTTGTGACTTTTACTAATAAAAATAAATCTGCCT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 AAAGTCAGCCAATAAGTCTTTTCCTATTTGTGACTTTTACTAATAAAAATAAATCTGCCT 960

Qy        961 GTAAATTATCTTGAAGTCCTTTACCTGGAACAAGCACTCTCTTTTTCACCACATAGTTTT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GTAAATTATCTTGAAGTCCTTTACCTGGAACAAGCACTCTCTTTTTCACCACATAGTTTT 1020

Qy       1021 AACTTGACTTTCAAGATAATTTTCAGGGTTTTTGTTGTTGTTGTTTTTTGTTTGTTTGTT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AACTTGACTTTCAAGATAATTTTCAGGGTTTTTGTTGTTGTTGTTTTTTGTTTGTTTGTT 1080

Qy       1081 TTGGTGGGAGAGGGGAGGGATGCCTGGGAAGTGGTTAACAACTTTTTTCAAGTCACTTTA 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TTGGTGGGAGAGGGGAGGGATGCCTGGGAAGTGGTTAACAACTTTTTTCAAGTCACTTTA 1140

Qy       1141 CTAAACAAACTTTTGTAAATAGACCTTACCTTCTATTTTCGAGTTTCATTTATATTTTGC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 CTAAACAAACTTTTGTAAATAGACCTTACCTTCTATTTTCGAGTTTCATTTATATTTTGC 1200

Qy       1201 AGTGTAGCCAGCCTCATCAAAGAGCTGACTTACTCATTTGACTTTTGCACTGACTGTATT 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AGTGTAGCCAGCCTCATCAAAGAGCTGACTTACTCATTTGACTTTTGCACTGACTGTATT 1260

Qy       1261 ATCTGGGTATCTGCTGTGTCTGCACTTCATGGTAAACGGGATCTAAAATGCCTGGTGGCT 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 ATCTGGGTATCTGCTGTGTCTGCACTTCATGGTAAACGGGATCTAAAATGCCTGGTGGCT 1320

Qy       1321 TTTCACAAAAAGCAGATTTTCTTCATGTACTGTGATGTCTGATGCAATGCATCCTAGAAC 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 TTTCACAAAAAGCAGATTTTCTTCATGTACTGTGATGTCTGATGCAATGCATCCTAGAAC 1380

Qy       1381 AAACTGGCCATTTGCTAGTTTACTCTAAAGACTAAACATAGTCTTGGTGTGTGTGGTCTT 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 AAACTGGCCATTTGCTAGTTTACTCTAAAGACTAAACATAGTCTTGGTGTGTGTGGTCTT 1440

Qy       1441 ACTCATCTTCTAGTACCTTTAAGGACAAATCCTAAGGACTTGGACACTTGCAATAAAGAA 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 ACTCATCTTCTAGTACCTTTAAGGACAAATCCTAAGGACTTGGACACTTGCAATAAAGAA 1500

Qy       1501 ATTTTATTTTAAACCCAAGCCTCCCTGGATTGATAATATATACACATTTGTCAGCATTTC 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 ATTTTATTTTAAACCCAAGCCTCCCTGGATTGATAATATATACACATTTGTCAGCATTTC 1560

Qy       1561 CGGTCGTGGTGAGAGGCAGCTGTTTGAGCTCCAATATGTGCAGCTTTGAACTAGGGCTGG 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 CGGTCGTGGTGAGAGGCAGCTGTTTGAGCTCCAATATGTGCAGCTTTGAACTAGGGCTGG 1620

Qy       1621 GGTTGTGGGTGCCTCTTCTGAAAGGTCTAACCATTATTGGATAACTGGCTTTTTTCTTCC 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 GGTTGTGGGTGCCTCTTCTGAAAGGTCTAACCATTATTGGATAACTGGCTTTTTTCTTCC 1680

Qy       1681 TATGTCCTCTTTGGAATGTAACAATAAAAATAATTTTTGAAACATCAA 1728
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 TATGTCCTCTTTGGAATGTAACAATAAAAATAATTTTTGAAACATCAA 1728
```

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RESULT 4
AAC91485
ID   AAC91485 standard; cDNA; 1728 BP.
XX
AC   AAC91485;
XX
DT   21-MAR-2001  (first entry)
XX
DE   Human PRO1375 cDNA.
XX
KW   Human; PRO; antiinflammatory; dermatological; antiarthritic;
KW   antirheumatic; cardiant; antianaemic; immunosuppressive; antithyroid;
KW   antidiabetic; nootropic; neuroprotective; hepatotropic; virucide;
KW   antiallergic; antiasthmatic; immune related disorder;
KW   hepatobiliary disease; autoimmune disease; allergy; ss.
XX
OS   Homo sapiens.
XX
PN   WO200073452-A2.
XX
PD   07-DEC-2000.
XX
PF   02-JUN-2000; 2000WO-US015264.
XX
PR   02-JUN-1999;   99WO-US012252.
PR   20-JUL-1999;   99US-0144732P.
PR   20-JUL-1999;   99US-0144758P.
PR   28-JUL-1999;   99US-0146222P.
PR   01-SEP-1999;   99WO-US020111.
PR   15-SEP-1999;   99WO-US021090.
PR   15-SEP-1999;   99WO-US021547.
PR   29-OCT-1999;   99US-0162506P.
PR   30-NOV-1999;   99WO-US028313.
PR   01-DEC-1999;   99WO-US028634.
PR   02-DEC-1999;   99WO-US028551.
PR   02-DEC-1999;   99WO-US028565.
PR   09-DEC-1999;   99US-0170262P.
PR   20-DEC-1999;   99WO-US030911.
PR   05-JAN-2000; 2000WO-US000219.
PR   06-JAN-2000; 2000WO-US000376.
PR   11-FEB-2000; 2000WO-US003565.
PR   18-FEB-2000; 2000WO-US004341.
PR   18-FEB-2000; 2000WO-US004342.
PR   22-FEB-2000; 2000WO-US004414.
PR   24-FEB-2000; 2000WO-US004914.
PR   24-FEB-2000; 2000WO-US005004.
PR   01-MAR-2000; 2000WO-US005601.
PR   02-MAR-2000; 2000WO-US005841.
PR   03-MAR-2000; 2000US-0187202P.
PR   15-MAR-2000; 2000WO-US006884.
PR   20-MAR-2000; 2000WO-US007377.
PR   21-MAR-2000; 2000WO-US007532.
PR   30-MAR-2000; 2000WO-US008439.
PR   17-MAY-2000; 2000WO-US013705.
PR   22-MAY-2000; 2000WO-US014042.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Ashkenazi AJ,  Baker KP,  Chan B,  Goddard A,  Godowski PJ;
PI   Gurney AL,  Hebert C,  Henzel W,  Kabakoff RC,  Shelton DL,  Tumas D;
PI   Watanabe CK,  Wood WI;
XX
DR   WPI; 2001-025253/03.
DR   P-PSDB; AAB50926.
XX
PT   Thirty three nucleic acids encoding PRO polypeptides which are useful in
PT   the diagnosis and treatment of immune related disorders, e.g. systemic
PT   lupus erythematosis, rheumatoid arthritis, osteoarthritis, thyroiditis
PT   and diabetes mellitus.
XX
PS   Claim 48; Fig 49; 218pp; English.
```

XX
CC The present sequence is one of thirty three nucleic acids encoding PRO
CC polypeptides. The PRO polypeptides, anti-PRO antibodies, agonists and
CC antagonists are useful for treating and diagnosing immune related
CC disorders such as systemic lupus erythematosus, rheumatoid arthritis,
CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,
CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic
CC anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus,
CC immune-mediated renal disease, demyelinating diseases of the central and
CC peripheral nervous systems (such as multiple sclerosis, idiopathic
CC demyelinating polyneuropathy or Guillain-Barre syndrome, and chronic
CC inflammatory demyelinating polyneuropathy), hepatobiliary diseases (such
CC as infectious, autoimmune chronic active hepatitis, primary biliary
CC cirrhosis, granulomatous hepatitis and sclerosing cholangitis),
CC inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's
CC disease, autoimmune or immune-mediated skin diseases (such as bullous
CC skin diseases, erythema multiforme, contact dermatitis, psoriasis),
CC allergic diseases such as asthma, allergic rhinitis, atopic dermatitis,
CC food hypersensitivity and urticaria), immunological diseases of the lung
CC (such as eosinophilic pneumonias, idiopathic pulmonary fibrosis and
CC hypersensitivity pneumonitis), transplantation associated diseases
CC including graft rejection and graft-versus-host diseases
XX
SQ Sequence 1728 BP; 438 A; 360 C; 390 G; 540 T; 0 U; 0 Other;

Query Match 100.0%; Score 1728; DB 5; Length 1728;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1728; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy    1 CAGCCGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCC 60
Db    1 CAGCCGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCC 60

Qy   61 GGTCGCGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCCAGCGATGGCGACCCTGTGGGG 120
Db   61 GGTCGCGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCCAGCGATGGCGACCCTGTGGGG 120

Qy  121 AGGCCTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTTCCGTGCTGCT 180
Db  121 AGGCCTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTTCCGTGCTGCT 180

Qy  181 GCTGGCGCAGCTGTCAGACGCCGCCAAGAATTTCGAGGATGTCAGATGTAAATGTATCTG 240
Db  181 GCTGGCGCAGCTGTCAGACGCCGCCAAGAATTTCGAGGATGTCAGATGTAAATGTATCTG 240

Qy  241 CCCTCCCTATAAAGAAAATTCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTG 300
Db  241 CCCTCCCTATAAAGAAAATTCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTG 300

Qy  301 TGATTGCCTTCATGTTGTGGAGCCCATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTG 360
Db  301 TGATTGCCTTCATGTTGTGGAGCCCATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTG 360

Qy  361 TCTACGCTGTGAATGCAAATATGAAGAAAGAAGCTCTGTCACAATCAAGGTTACCATTAT 420
Db  361 TCTACGCTGTGAATGCAAATATGAAGAAAGAAGCTCTGTCACAATCAAGGTTACCATTAT 420

Qy  421 AATTTATCTCTCCATTTTGGGCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGA 480
Db  421 AATTTATCTCTCCATTTTGGGCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGA 480

Qy  481 GCCCATACTGAAGAGGCGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATAT 540
Db  481 GCCCATACTGAAGAGGCGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATAT 540

Qy  541 TGGGGATCACCAGCCTTTTGCAAATGCACACGATGTGCTAGCCCGCTCCCGCAGTCGAGC 600
Db  541 TGGGGATCACCAGCCTTTTGCAAATGCACACGATGTGCTAGCCCGCTCCCGCAGTCGAGC 600

Qy  601 CAACGTGCTGAACAAGGTAGAATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCA 660
Db  601 CAACGTGCTGAACAAGGTAGAATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCA 660

Qy  661 GCGAAAGTCTGTCTTTGACCGGCATGTTGTCCTCAGCTAATTGGGAATTGAATTCAAGGT 720
Db  661 GCGAAAGTCTGTCTTTGACCGGCATGTTGTCCTCAGCTAATTGGGAATTGAATTCAAGGT 720

Qy  721 GACTAGAAAGAAACAGGCAGACAACTGGAAAGAACTGACTGGGTTTTGCTGGGTTTCATT 780
Db  721 GACTAGAAAGAAACAGGCAGACAACTGGAAAGAACTGACTGGGTTTTGCTGGGTTTCATT 780

Qy  781 TTAATACCTTGTTGATTTCACCAACTGTTGCTGGAAGATTCAAAACTGGAAGCAAAAACT 840
Db  781 TTAATACCTTGTTGATTTCACCAACTGTTGCTGGAAGATTCAAAACTGGAAGCAAAAACT 840

Qy  841 TGCTTGATTTTTTTTTCTTGTTAACGTAATAATAGAGACATTTTTAAAAGCACACAGCTC 900
Db  841 TGCTTGATTTTTTTTTCTTGTTAACGTAATAATAGAGACATTTTTAAAAGCACACAGCTC 900

Qy  901 AAAGTCAGCCAATAAGTCTTTTCCTATTTGTGACTTTTACTAATAAAAATAAATCTGCCT 960
Db  901 AAAGTCAGCCAATAAGTCTTTTCCTATTTGTGACTTTTACTAATAAAAATAAATCTGCCT 960

Qy  961 GTAAATTATCTTGAAGTCCTTTACCTGGAACAAGCACTCTCTTTTTCACCACATAGTTTT 1020
Db  961 GTAAATTATCTTGAAGTCCTTTACCTGGAACAAGCACTCTCTTTTTCACCACATAGTTTT 1020

Qy 1021 AACTTGACTTTCAAGATAATTTTCAGGGTTTTTGTTGTTGTTGTTTTTTGTTTGTTTGTT 1080
Db 1021 AACTTGACTTTCAAGATAATTTTCAGGGTTTTTGTTGTTGTTGTTTTTTGTTTGTTTGTT 1080

Qy 1081 TTGGTGGGAGAGGGGAGGGATGCCTGGGAAGTGGTTAACAACTTTTTTCAAGTCACTTTA 1140
Db 1081 TTGGTGGGAGAGGGGAGGGATGCCTGGGAAGTGGTTAACAACTTTTTTCAAGTCACTTTA 1140

Qy 1141 CTAAACAAACTTTTGTAAATAGACCTTACCTTCTATTTTCGAGTTTCATTTATATTTTGC 1200
Db 1141 CTAAACAAACTTTTGTAAATAGACCTTACCTTCTATTTTCGAGTTTCATTTATATTTTGC 1200

Qy 1201 AGTGTAGCCAGCCTCATCAAAGAGCTGACTTACTCATTTGACTTTTGCACTGACTGTATT 1260
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Qy 1261 ATCTGGGTATCTGCTGTGTCTGCACTTCATGGTAAACGGGATCTAAAATGCCTGGTGGCT 1320
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Qy 1381 AAACTGGCCATTTGCTAGTTTACTCTAAAGACTAAACATAGTCTTGGTGTGTGTGGTCTT 1440
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Qy 1441 ACTCATCTTCTAGTACCTTTAAGGACAAATCCTAAGGACTTGGACACTTGCAATAAAGAA 1500
Db 1441 ACTCATCTTCTAGTACCTTTAAGGACAAATCCTAAGGACTTGGACACTTGCAATAAAGAA 1500

Qy 1501 ATTTTATTTTAAACCCAAGCCTCCCTGGATTGATAATATATACACATTTGTCAGCATTTC 1560
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Qy 1561 CGGTCGTGGTGAGAGGCAGCTGTTTGAGCTCCAATATGTGCAGCTTTGAACTAGGGCTGG 1620
Db 1561 CGGTCGTGGTGAGAGGCAGCTGTTTGAGCTCCAATATGTGCAGCTTTGAACTAGGGCTGG 1620

Qy 1621 GGTTGTGGGTGCCTCTTCTGAAAGGTCTAACCATTATTGGATAACTGGCTTTTTTCTTCC 1680
Db 1621 GGTTGTGGGTGCCTCTTCTGAAAGGTCTAACCATTATTGGATAACTGGCTTTTTTCTTCC 1680

Qy 1681 TATGTCCTCTTTGGAATGTAACAATAAAAATAATTTTTGAAACATCAA 1728
Db 1681 TATGTCCTCTTTGGAATGTAACAATAAAAATAATTTTTGAAACATCAA 1728
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AAF44254
ID   AAF44254 standard; cDNA; 1728 BP.
XX
AC   AAF44254;
XX
DT   02-APR-2001  (first entry)
XX
DE   Human PRO1375 (UNQ712) nucleotide sequence SEQ ID NO:417.
XX
KW   Human; secreted and transmembrane protein; PRO; cytostatic; cell death;
KW   cancer; chromosomal mapping; gene mapping; tissue typing;
KW   diagnostic assay; ss.
XX
OS   Homo sapiens.
XX
PN   WO200073454-A1.
XX
PD   07-DEC-2000.
XX
PF   30-MAR-2000; 2000WO-US008439.
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PR   02-JUN-1999;   99WO-US012252.
PR   23-JUN-1999;   99US-0141037P.
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PR   28-JUL-1999;   99US-0146222P.
PR   17-AUG-1999;   99US-0149396P.
PR   15-SEP-1999;   99WO-US021090.
PR   15-SEP-1999;   99WO-US021547.
PR   08-OCT-1999;   99US-0158663P.
PR   30-NOV-1999;   99WO-US028313.
PR   01-DEC-1999;   99WO-US028301.
PR   16-DEC-1999;   99WO-US030095.
PR   20-DEC-1999;   99WO-US030911.
PR   05-JAN-2000; 2000WO-US000219.
PR   06-JAN-2000; 2000WO-US000376.
PR   11-FEB-2000; 2000WO-US003565.
PR   18-FEB-2000; 2000WO-US004341.
PR   22-FEB-2000; 2000WO-US004414.
PR   24-FEB-2000; 2000WO-US004914.
PR   24-FEB-2000; 2000WO-US005004.
PR   02-MAR-2000; 2000WO-US005841.
PR   15-MAR-2000; 2000WO-US006884.
PR   20-MAR-2000; 2000WO-US007377.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Ashkenazi AJ,  Baker KP,  Botstein D,  Desnoyers L,  Eaton DL;
PI   Ferrara N,  Fong S,  Gerber H,  Gerritsen ME,  Goddard A,  Godowski PJ;
PI   Grimaldi CJ,  Gurney AL,  Kljavin IJ,  Napier MA,  Pan J,  Paoni NF;
PI   Roy MA,  Stewart TA,  Tumas D,  Watanabe CK,  Williams PM,  Wood WI;
PI   Zhang Z;
XX
DR   WPI; 2001-032160/04.
DR   P-PSDB; AAB65285.
XX
PT   PRO polynucleotides used to produce polypeptides used to target bioactive
PT   molecules such as toxins, radiolabels or antibodies, to specific cells,
PT   to cause targeted cell death.
XX
PS   Claim 2; Fig 299; 935pp; English.
XX
CC   The present invention describes human secreted and transmembrane PRO
CC   proteins. The PRO proteins have cytostatic activity. The PRO proteins can
CC   be used for targeted delivery of bioactive molecules, such as toxins,
CC   radiolabels or antibodies, that cause cell death. PRO nucleotide
CC   sequences, and their fragments, can be used as hybridisation probes, in
CC   chromosomal and gene mapping, and in the generation of anti-sense RNA and
CC   DNA. They may also be used to produce transgenic animals which are used
CC   to develop and screen therapeutically useful reagents. The PRO nucleotide
CC   and protein sequence can be used for tissue typing and in treating
CC   cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to
CC   AAF44470 represent PCR primers and hybridisation probes used in the
CC   isolation of human PRO sequences. AAF44087 to AAF44269 and AAB65154 to
CC   AAB65300 represent human PRO polynucleotide and protein sequences given
CC   in the exemplification of the present invention
XX
SQ   Sequence 1728 BP; 438 A; 360 C; 390 G; 540 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 1728;  DB 5;  Length 1728;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1728;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CAGCCGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCC 60
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Db          1 CAGCCGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCC 60

Qy         61 GGTCGCGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCCAGCGATGGCGACCCTGTGGGG 120
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Qy        121 AGGCCTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTTCCGTGCTGCT 180
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Db        121 AGGCCTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTTCCGTGCTGCT 180

Qy        181 GCTGGCGCAGCTGTCAGACGCCGCCAAGAATTTCGAGGATGTCAGATGTAAATGTATCTG 240
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Db        181 GCTGGCGCAGCTGTCAGACGCCGCCAAGAATTTCGAGGATGTCAGATGTAAATGTATCTG 240

Qy        241 CCCTCCCTATAAAGAAAATTCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTG 300
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Db        241 CCCTCCCTATAAAGAAAATTCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTG 300

Qy        301 TGATTGCCTTCATGTTGTGGAGCCCATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGATTGCCTTCATGTTGTGGAGCCCATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTG 360

Qy        361 TCTACGCTGTGAATGCAAATATGAAGAAAGAAGCTCTGTCACAATCAAGGTTACCATTAT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TCTACGCTGTGAATGCAAATATGAAGAAAGAAGCTCTGTCACAATCAAGGTTACCATTAT 420

Qy        421 AATTTATCTCTCCATTTTGGGCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AATTTATCTCTCCATTTTGGGCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGA 480

Qy        481 GCCCATACTGAAGAGGCGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATAT 540
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Db        481 GCCCATACTGAAGAGGCGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATAT 540

Qy        541 TGGGGATCACCAGCCTTTTGCAAATGCACACGATGTGCTAGCCCGCTCCCGCAGTCGAGC 600
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Db        541 TGGGGATCACCAGCCTTTTGCAAATGCACACGATGTGCTAGCCCGCTCCCGCAGTCGAGC 600

Qy        601 CAACGTGCTGAACAAGGTAGAATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCA 660
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Db        601 CAACGTGCTGAACAAGGTAGAATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCA 660

Qy        661 GCGAAAGTCTGTCTTTGACCGGCATGTTGTCCTCAGCTAATTGGGAATTGAATTCAAGGT 720
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Qy        721 GACTAGAAAGAAACAGGCAGACAACTGGAAAGAACTGACTGGGTTTTGCTGGGTTTCATT 780
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Db        721 GACTAGAAAGAAACAGGCAGACAACTGGAAAGAACTGACTGGGTTTTGCTGGGTTTCATT 780

Qy        781 TTAATACCTTGTTGATTTCACCAACTGTTGCTGGAAGATTCAAAACTGGAAGCAAAAACT 840
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Db        781 TTAATACCTTGTTGATTTCACCAACTGTTGCTGGAAGATTCAAAACTGGAAGCAAAAACT 840

Qy        841 TGCTTGATTTTTTTTTCTTGTTAACGTAATAATAGAGACATTTTTAAAAGCACACAGCTC 900
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Db        841 TGCTTGATTTTTTTTTCTTGTTAACGTAATAATAGAGACATTTTTAAAAGCACACAGCTC 900
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Qy        901 AAAGTCAGCCAATAAGTCTTTTCCTATTTGTGACTTTTACTAATAAAAATAAATCTGCCT 960
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Db        901 AAAGTCAGCCAATAAGTCTTTTCCTATTTGTGACTTTTACTAATAAAAATAAATCTGCCT 960

Qy        961 GTAAATTATCTTGAAGTCCTTTACCTGGAACAAGCACTCTCTTTTTCACCACATAGTTTT 1020
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Db        961 GTAAATTATCTTGAAGTCCTTTACCTGGAACAAGCACTCTCTTTTTCACCACATAGTTTT 1020

Qy       1021 AACTTGACTTTCAAGATAATTTTCAGGGTTTTTGTTGTTGTTGTTTTTTGTTTGTTTGTT 1080
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Db       1021 AACTTGACTTTCAAGATAATTTTCAGGGTTTTTGTTGTTGTTGTTTTTTGTTTGTTTGTT 1080

Qy       1081 TTGGTGGGAGAGGGGAGGGATGCCTGGGAAGTGGTTAACAACTTTTTTCAAGTCACTTTA 1140
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Db       1081 TTGGTGGGAGAGGGGAGGGATGCCTGGGAAGTGGTTAACAACTTTTTTCAAGTCACTTTA 1140

Qy       1141 CTAAACAAACTTTTGTAAATAGACCTTACCTTCTATTTTCGAGTTTCATTTATATTTTGC 1200
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Db       1141 CTAAACAAACTTTTGTAAATAGACCTTACCTTCTATTTTCGAGTTTCATTTATATTTTGC 1200

Qy       1201 AGTGTAGCCAGCCTCATCAAAGAGCTGACTTACTCATTTGACTTTTGCACTGACTGTATT 1260
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Db       1201 AGTGTAGCCAGCCTCATCAAAGAGCTGACTTACTCATTTGACTTTTGCACTGACTGTATT 1260

Qy       1261 ATCTGGGTATCTGCTGTGTCTGCACTTCATGGTAAACGGGATCTAAAATGCCTGGTGGCT 1320
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Db       1261 ATCTGGGTATCTGCTGTGTCTGCACTTCATGGTAAACGGGATCTAAAATGCCTGGTGGCT 1320

Qy       1321 TTTCACAAAAAGCAGATTTTCTTCATGTACTGTGATGTCTGATGCAATGCATCCTAGAAC 1380
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Qy       1381 AAACTGGCCATTTGCTAGTTTACTCTAAAGACTAAACATAGTCTTGGTGTGTGTGGTCTT 1440
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Qy       1441 ACTCATCTTCTAGTACCTTTAAGGACAAATCCTAAGGACTTGGACACTTGCAATAAAGAA 1500
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Db       1441 ACTCATCTTCTAGTACCTTTAAGGACAAATCCTAAGGACTTGGACACTTGCAATAAAGAA 1500

Qy       1501 ATTTTATTTTAAACCCAAGCCTCCCTGGATTGATAATATATACACATTTGTCAGCATTTC 1560
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Db       1621 GGTTGTGGGTGCCTCTTCTGAAAGGTCTAACCATTATTGGATAACTGGCTTTTTTCTTCC 1680

Qy       1681 TATGTCCTCTTTGGAATGTAACAATAAAAATAATTTTTGAAACATCAA 1728
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Db       1681 TATGTCCTCTTTGGAATGTAACAATAAAAATAATTTTTGAAACATCAA 1728
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RESULT 6
ABX77979
ID ABX77979 standard; cDNA; 1728 BP.
XX
AC ABX77979;
XX
DT 14-APR-2003 (first entry)
XX
DE Human PRO polynucleotide #132.
XX
KW Human; PRO; gene; ss; cytostatic; tumour; cancer; breast; lung; stomach;
KW liver; horse; cow; dog; cat; sheep; pig; goat; rabbit; ADEPT;
KW antibody-dependent enzyme mediated prodrug therapy.
XX
OS Homo sapiens.
XX

PN US2003027163-A1.
XX
PD 06-FEB-2003.
XX
PF 15-NOV-2001; 2001US-00997666.
XX
PR 16-JUN-1997; 97US-0049787P.
PR 17-OCT-1997; 97US-0062250P.
PR 05-NOV-1997; 97WO-US020069.
PR 12-NOV-1997; 97US-0065186P.
PR 13-NOV-1997; 97US-0065311P.
PR 24-NOV-1997; 97US-0066770P.
PR 25-FEB-1998; 98US-0075945P.
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PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
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PR 30-MAY-2000; 2000WO-US014941.
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PR 23-JUN-2000; 2000US-0213637P.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
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PR 24-AUG-2000; 2000WO-US023328.
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Query Match 100.0%; Score 1728; DB 7; Length 1728;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1728; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 7
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ID ABX80391 standard; DNA; 1728 BP.
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AC ABX80391;
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DT 28-APR-2003 (first entry)
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DE Novel human secreted or transmembrane protein PRO1385 DNA.
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KW Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;
KW cardiac insufficiency disorder; cancer; tumour; immune response;
KW adrenal cortical capillary endothelial growth; c-fos induction;
KW vascular endothelial growth factor inhibition; VEGF inhibition;
KW endothelial cell growth inhibitor; T-lymphocytes stimulation;
KW retinal neurons cell survival; rod photoreceptor cell survival;
KW retinal disorder; retinitis pigmentosum; kidney disorder;
KW mammalian kidney mesangial cell proliferation; Berger disease;
KW dermatitis; herpetiformis; Crohn's disease; chondrocyte proliferation;
KW chondrocyte redifferentiation; sports injury; arthritis; gene; ds.
XX
OS Homo sapiens.
XX
PN US2002132252-A1.
XX
PD 19-SEP-2002.
XX
PF 14-NOV-2001; 2001US-00990442.
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PR 16-JUN-1997; 97US-0049787P.
PR 17-OCT-1997; 97US-0062250P.
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PR 12-NOV-1997; 97US-0065186P.
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PR 30-NOV-1999; 99WO-US028313.
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PR 20-DEC-1999; 99WO-US030911.
PR 06-JAN-2000; 2000WO-US000219.
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PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
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PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
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PR 28-FEB-2001; 2001WO-US006520.
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PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 28-AUG-2001; 2001US-00941992.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
PI Zhang Z;

XX
DR WPI; 2003-247083/24.
DR P-PSDB; ABU59179.
XX
PT Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346
PT and PRO1375, which stimulate proliferation of stimulated T-lymphocytes
PT are therapeutically useful for enhancing immune response and in cancer
PT treatments.
XX
PS Claim 2; Fig 301; 648pp; English.
XX
CC The invention describes an isolated human PRO polypeptide. The PRO
CC polypeptides are useful in detecting PRO polypeptides in a sample, in
CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and
CC in modulating at least one biological activity of a cell expressing a PRO
CC polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus
CC useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186
CC stimulate adrenal cortical capillary endothelial growth, and PRO536,
CC PRO943, PRO828, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126,
CC PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus
CC useful for treating conditions or disorders where angiogenesis would be
CC beneficial, e.g. wound healing and antagonist of this polypeptide are
CC useful for treating cancerous tumours. PRO812 inhibits vascular
CC endothelial growth factor (VEGF) stimulated proliferation of endothelial
CC cells and is thus useful for inhibiting endothelial cell growth in
CC mammals which would be beneficial in inhibiting tumour growth. PRO826,
CC PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of
CC stimulated T-lymphocytes and are therapeutically useful for enhancing
CC immune response. PRO828, PRO826, PRO1068 or PRO1132 enhance survival of
CC retinal neurons cells (PRO1132 is also enhances survival/proliferation of
CC rod photoreceptor cells) and therefore are useful for treating retinal
CC disorders of injuries, e.g. retinitis pigmentosum, AMD. PRO819, PRO813
CC and PRO11066 induce proliferation of mammalian kidney mesangial cells,
CC and therefore are useful for treating kidney disorders associated with
CC decreased mesangial cell function such as Berger disease or other
CC nephropathies associated with dermatitis, herpetiformis or Crohn's
CC disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the
CC proliferation and/or redifferentiation of chondrocytes in culture and are
CC thus useful for treating sports injuries, and arthritis. This sequence
CC represents a novel human PRO protein polynucleotide
XX
SQ Sequence 1728 BP; 438 A; 360 C; 390 G; 540 T; 0 U; 0 Other;

Query Match 100.0%; Score 1728; DB 7; Length 1728;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1728; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DT 26-JUN-2003 (first entry)
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KW Human; ss; gene; PRO; secreted protein; transmembrane protein;
KW cardiac insufficiency disorders; angiogenesis; wound healing;
KW cancerous tumour; immune response; retinal disorder; sight loss;
KW retinitis pigmentosum; age-related macular degeneration; AMD;
KW kidney disorder; Berger disease; nephropathy; dermatitis; herpetiformis;
KW Crohn's disease; sports injury; arthritis.
XX
OS Homo sapiens.
XX
PN US2003032023-A1.
XX
PD 13-FEB-2003.
XX
PF 14-NOV-2001; 2001US-00990711.
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PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 28-AUG-2001; 2001US-00941992.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
PI Zhang Z;
XX
DR WPI; 2003-288106/28.
DR P-PSDB; ABU60609.
XX
PT New transmembrane polypeptides and nucleic acids encoding the
PT polypeptides, useful in gene therapy, in chromosome identification, as
PT chromosome markers, or in generating probes.
XX
PS Claim 2; Fig 299; 650pp; English.
XX
CC The invention discloses isolated PRO secreted/transmembrane polypeptides
CC comprising a sequence without signal peptide and the nucleic acid
CC encoding them. The polypeptides can be used to raise antibodies that
CC specifically bind to the PRO polypeptide, for linking a bioactive
CC molecule to a cell expressing a PRO protein and for modulating at least
CC one biological activity of a cell. The PRO polypeptides or
CC polynucleotides are also useful in gene therapy, in chromosome
CC identification, as chromosome markers, or in generating probes. The PRO
CC polypeptides are useful as molecular markers for protein electrophoresis,
CC and the isolated nucleic acids may be used for recombinantly expressing
CC those markers. The PRO polypeptides and nucleic acids may also be used in
CC tissue typing. Anti-PRO antibodies are useful in diagnostic assays for
CC PRO, and in affinity purification of PRO from recombinant cell culture or
CC natural sources. The sequences presented in ABX90083-ABX90468 are the
CC genes encoding, the primers amplifying and the probes detecting the PRO
CC polynucleotides of the invention. Note: The sequence data for this patent
CC is also available in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html
XX
SQ Sequence 1728 BP; 438 A; 360 C; 390 G; 540 T; 0 U; 0 Other;

Query Match 100.0%; Score 1728; DB 7; Length 1728;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1728; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGCCGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCC 60
Db 1 CAGCCGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCC 60

Qy 61 GGTCGCGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCCAGCGATGGCGACCCTGTGGGG 120
Db 61 GGTCGCGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCCAGCGATGGCGACCCTGTGGGG 120

Qy 121 AGGCCTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTTCCGTGCTGCT 180
Db 121 AGGCCTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTTCCGTGCTGCT 180

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Qy       181 GCTGGCGCAGCTGTCAGACGCCGCCAAGAATTTCGAGGATGTCAGATGTAAATGTATCTG 240
Db       181 GCTGGCGCAGCTGTCAGACGCCGCCAAGAATTTCGAGGATGTCAGATGTAAATGTATCTG 240

Qy       241 CCCTCCCTATAAAGAAAATTCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTG 300
Db       241 CCCTCCCTATAAAGAAAATTCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTG 300

Qy       301 TGATTGCCTTCATGTTGTGGAGCCCATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTG 360
Db       301 TGATTGCCTTCATGTTGTGGAGCCCATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTG 360

Qy       361 TCTACGCTGTGAATGCAAATATGAAGAAAGAAGCTCTGTCACAATCAAGGTTACCATTAT 420
Db       361 TCTACGCTGTGAATGCAAATATGAAGAAAGAAGCTCTGTCACAATCAAGGTTACCATTAT 420

Qy       421 AATTTATCTCTCCATTTTGGGCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGA 480
Db       421 AATTTATCTCTCCATTTTGGGCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGA 480

Qy       481 GCCCATACTGAAGAGGCGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATAT 540
Db       481 GCCCATACTGAAGAGGCGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATAT 540

Qy       541 TGGGGATCACCAGCCTTTTGCAAATGCACACGATGTGCTAGCCCGCTCCCGCAGTCGAGC 600
Db       541 TGGGGATCACCAGCCTTTTGCAAATGCACACGATGTGCTAGCCCGCTCCCGCAGTCGAGC 600

Qy       601 CAACGTGCTGAACAAGGTAGAATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCA 660
Db       601 CAACGTGCTGAACAAGGTAGAATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCA 660

Qy       661 GCGAAAGTCTGTCTTTGACCGGCATGTTGTCCTCAGCTAATTGGGAATTGAATTCAAGGT 720
Db       661 GCGAAAGTCTGTCTTTGACCGGCATGTTGTCCTCAGCTAATTGGGAATTGAATTCAAGGT 720

Qy       721 GACTAGAAAGAAACAGGCAGACAACTGGAAAGAACTGACTGGGTTTTGCTGGGTTTCATT 780
Db       721 GACTAGAAAGAAACAGGCAGACAACTGGAAAGAACTGACTGGGTTTTGCTGGGTTTCATT 780

Qy       781 TTAATACCTTGTTGATTTCACCAACTGTTGCTGGAAGATTCAAAACTGGAAGCAAAAACT 840
Db       781 TTAATACCTTGTTGATTTCACCAACTGTTGCTGGAAGATTCAAAACTGGAAGCAAAAACT 840

Qy       841 TGCTTGATTTTTTTTTCTTGTTAACGTAATAATAGAGACATTTTTAAAAGCACACAGCTC 900
Db       841 TGCTTGATTTTTTTTTCTTGTTAACGTAATAATAGAGACATTTTTAAAAGCACACAGCTC 900

Qy       901 AAAGTCAGCCAATAAGTCTTTTCCTATTTGTGACTTTTACTAATAAAAATAAATCTGCCT 960
Db       901 AAAGTCAGCCAATAAGTCTTTTCCTATTTGTGACTTTTACTAATAAAAATAAATCTGCCT 960

Qy       961 GTAAATTATCTTGAAGTCCTTTACCTGGAACAAGCACTCTCTTTTTCACCACATAGTTTT 1020
Db       961 GTAAATTATCTTGAAGTCCTTTACCTGGAACAAGCACTCTCTTTTTCACCACATAGTTTT 1020

Qy      1021 AACTTGACTTTCAAGATAATTTTCAGGGTTTTTGTTGTTGTTGTTTTTTGTTTGTTTGTT 1080
Db      1021 AACTTGACTTTCAAGATAATTTTCAGGGTTTTTGTTGTTGTTGTTTTTTGTTTGTTTGTT 1080

Qy      1081 TTGGTGGGAGAGGGGAGGGATGCCTGGGAAGTGGTTAACAACTTTTTTCAAGTCACTTTA 1140
Db      1081 TTGGTGGGAGAGGGGAGGGATGCCTGGGAAGTGGTTAACAACTTTTTTCAAGTCACTTTA 1140

Qy      1141 CTAAACAAACTTTTGTAAATAGACCTTACCTTCTATTTTCGAGTTTCATTTATATTTTGC 1200
Db      1141 CTAAACAAACTTTTGTAAATAGACCTTACCTTCTATTTTCGAGTTTCATTTATATTTTGC 1200

Qy      1201 AGTGTAGCCAGCCTCATCAAAGAGCTGACTTACTCATTTGACTTTTGCACTGACTGTATT 1260
Db      1201 AGTGTAGCCAGCCTCATCAAAGAGCTGACTTACTCATTTGACTTTTGCACTGACTGTATT 1260

Qy      1261 ATCTGGGTATCTGCTGTGTCTGCACTTCATGGTAAACGGGATCTAAAATGCCTGGTGGCT 1320
Db      1261 ATCTGGGTATCTGCTGTGTCTGCACTTCATGGTAAACGGGATCTAAAATGCCTGGTGGCT 1320

Qy      1321 TTTCACAAAAAGCAGATTTTCTTCATGTACTGTGATGTCTGATGCAATGCATCCTAGAAC 1380
Db      1321 TTTCACAAAAAGCAGATTTTCTTCATGTACTGTGATGTCTGATGCAATGCATCCTAGAAC 1380

Qy      1381 AAACTGGCCATTTGCTAGTTTACTCTAAAGACTAAACATAGTCTTGGTGTGTGTGGTCTT 1440
Db      1381 AAACTGGCCATTTGCTAGTTTACTCTAAAGACTAAACATAGTCTTGGTGTGTGTGGTCTT 1440

Qy      1441 ACTCATCTTCTAGTACCTTTAAGGACAAATCCTAAGGACTTGGACACTTGCAATAAAGAA 1500
Db      1441 ACTCATCTTCTAGTACCTTTAAGGACAAATCCTAAGGACTTGGACACTTGCAATAAAGAA 1500

Qy      1501 ATTTTATTTTAAACCCAAGCCTCCCTGGATTGATAATATATACACATTTGTCAGCATTTC 1560
Db      1501 ATTTTATTTTAAACCCAAGCCTCCCTGGATTGATAATATATACACATTTGTCAGCATTTC 1560

Qy      1561 CGGTCGTGGTGAGAGGCAGCTGTTTGAGCTCCAATATGTGCAGCTTTGAACTAGGGCTGG 1620
Db      1561 CGGTCGTGGTGAGAGGCAGCTGTTTGAGCTCCAATATGTGCAGCTTTGAACTAGGGCTGG 1620

Qy      1621 GGTTGTGGGTGCCTCTTCTGAAAGGTCTAACCATTATTGGATAACTGGCTTTTTTCTTCC 1680
Db      1621 GGTTGTGGGTGCCTCTTCTGAAAGGTCTAACCATTATTGGATAACTGGCTTTTTTCTTCC 1680

Qy      1681 TATGTCCTCTTTGGAATGTAACAATAAAAATAATTTTTGAAACATCAA 1728
Db      1681 TATGTCCTCTTTGGAATGTAACAATAAAAATAATTTTTGAAACATCAA 1728
```

RESULT 10
ABX64214
ID ABX64214 standard; cDNA; 1728 BP.
XX
AC ABX64214;
XX
DT 26-FEB-2003 (first entry)
XX
DE cDNA encoding human PRO1375 polypeptide.
XX
KW Human; PRO polypeptide; secreted protein; transmembrane protein;
KW genetic disorder; antibacterial; immunosuppressive; transgenic;
KW gene therapy; gene; ss.
XX
OS Homo sapiens.
XX
PN US2002103125-A1.
XX
PD 01-AUG-2002.
XX
PF 20-NOV-2001; 2001US-00989731.
XX
PR 16-JUN-1997; 97US-0049787P.
PR 17-OCT-1997; 97US-0062250P.
PR 05-NOV-1997; 97WO-US020069.
PR 12-NOV-1997; 97US-0065186P.
PR 13-NOV-1997; 97US-0065311P.
PR 24-NOV-1997; 97US-0066770P.
PR 25-FEB-1998; 98US-0075945P.
PR 20-MAR-1998; 98US-0078910P.
PR 28-APR-1998; 98US-0083322P.
PR 07-MAY-1998; 98US-0084600P.
PR 28-MAY-1998; 98US-0087106P.
PR 02-JUN-1998; 98US-0087607P.
PR 02-JUN-1998; 98US-0087609P.
PR 02-JUN-1998; 98US-0087759P.
PR 03-JUN-1998; 98US-0087827P.
PR 04-JUN-1998; 98US-0088021P.
PR 04-JUN-1998; 98US-0088025P.
PR 04-JUN-1998; 98US-0088026P.
PR 04-JUN-1998; 98US-0088028P.

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PR 05-JUN-1998; 98US-0088217P.
PR 09-JUN-1998; 98US-0088655P.
PR 10-JUN-1998; 98US-0088734P.
PR 10-JUN-1998; 98US-0088738P.
PR 10-JUN-1998; 98US-0088742P.
PR 10-JUN-1998; 98US-0088810P.
PR 10-JUN-1998; 98US-0088824P.
PR 10-JUN-1998; 98US-0088826P.
PR 11-JUN-1998; 98US-0088858P.
PR 11-JUN-1998; 98US-0088861P.
PR 11-JUN-1998; 98US-0088876P.
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PR 16-JUN-1998; 98US-0089512P.
PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089532P.
PR 17-JUN-1998; 98US-0089538P.
PR 17-JUN-1998; 98US-0089598P.
PR 17-JUN-1998; 98US-0089599P.
PR 17-JUN-1998; 98US-0089600P.
PR 17-JUN-1998; 98US-0089653P.
PR 18-JUN-1998; 98US-0089801P.
PR 18-JUN-1998; 98US-0089907P.
PR 18-JUN-1998; 98US-0089908P.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 02-JUN-1999; 99WO-US012252.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 06-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.

PR 28-AUG-2001; 2001US-00941992.
XX
PA (GETH) GENENTECH LTD.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
PI Zhang Z;
XX
DR WPI; 2003-102117/09.
DR P-PSDB; ABU13991.
XX
PT Novel secreted and transmembrane polypeptide for modulating biological
PT activity of cell expressing the polypeptide, identifying agonists or
PT antagonists of polypeptide, and as molecular weight markers.
XX
PS Claim 2; Fig 299; 649pp; English.
XX
CC The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The PRO
CC polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides are useful for detecting other PRO polypeptides, for linking
CC bioactive molecules to cells expressing PRO polypeptides, for modulating
CC biological activities of cells expressing PRO polypeptides, and for for
CC identifying agonists or antagonists. The polynucleotide sequences
CC encoding PRO polypeptides are useful as hybridisation probes, in
CC chromosome and gene mapping, in the generation of antisense RNA and DNA,
CC in the preparation of PRO polypeptides, for generating transgenic animals
CC or knockout animals, to construct hybridisation probes for mapping the
CC gene which encodes the PRO polypeptide, and for the genetic analysis of
CC individuals with genetic disorders, in gene therapy, for chromosome
CC identification, as chromosome markers, and for generating probes for PCR,
CC Northern analysis, Southern analysis and Western analysis. The present
CC sequence encodes a human PRO polypeptide of the invention. Note: The
CC sequence data for this patent was obtained in electronic format directly
CC from the USPTO web site at seqdata.uspto.gov/psipsDIDEntry.html
XX
SQ Sequence 1728 BP; 438 A; 360 C; 390 G; 540 T; 0 U; 0 Other;

Query Match 100.0%; Score 1728; DB 7; Length 1728;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1728; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGCCGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCC 60
Db 1 CAGCCGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCC 60

Qy 61 GGTCGCGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCCAGCGATGGCGACCCTGTGGGG 120
Db 61 GGTCGCGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCCAGCGATGGCGACCCTGTGGGG 120

Qy 121 AGGCCTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTTCCGTGCTGCT 180
Db 121 AGGCCTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTTCCGTGCTGCT 180

Qy 181 GCTGGCGCAGCTGTCAGACGCCGCCAAGAATTTCGAGGATGTCAGATGTAAATGTATCTG 240
Db 181 GCTGGCGCAGCTGTCAGACGCCGCCAAGAATTTCGAGGATGTCAGATGTAAATGTATCTG 240

Qy 241 CCCTCCCTATAAAGAAAATTCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTG 300
Db 241 CCCTCCCTATAAAGAAAATTCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTG 300

Qy 301 TGATTGCCTTCATGTTGTGGAGCCCATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTG 360
Db 301 TGATTGCCTTCATGTTGTGGAGCCCATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTG 360

Qy 361 TCTACGCTGTGAATGCAAATATGAAGAAAGAAGCTCTGTCACAATCAAGGTTACCATTAT 420
Db 361 TCTACGCTGTGAATGCAAATATGAAGAAAGAAGCTCTGTCACAATCAAGGTTACCATTAT 420

Qy 421 AATTTATCTCTCCATTTTGGGCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGA 480

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Db        421 AATTTATCTCTCCATTTTGGGCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGA 480

Qy        481 GCCCATACTGAAGAGGCGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATAT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GCCCATACTGAAGAGGCGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATAT 540

Qy        541 TGGGGATCACCAGCCTTTTGCAAATGCACACGATGTGCTAGCCCGCTCCCGCAGTCGAGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TGGGGATCACCAGCCTTTTGCAAATGCACACGATGTGCTAGCCCGCTCCCGCAGTCGAGC 600

Qy        601 CAACGTGCTGAACAAGGTAGAATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAACGTGCTGAACAAGGTAGAATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCA 660

Qy        661 GCGAAAGTCTGTCTTTGACCGGCATGTTGTCCTCAGCTAATTGGGAATTGAATTCAAGGT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GCGAAAGTCTGTCTTTGACCGGCATGTTGTCCTCAGCTAATTGGGAATTGAATTCAAGGT 720

Qy        721 GACTAGAAAGAAACAGGCAGACAACTGGAAAGAACTGACTGGGTTTTGCTGGGTTTCATT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GACTAGAAAGAAACAGGCAGACAACTGGAAAGAACTGACTGGGTTTTGCTGGGTTTCATT 780

Qy        781 TTAATACCTTGTTGATTTCACCAACTGTTGCTGGAAGATTCAAAACTGGAAGCAAAAACT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TTAATACCTTGTTGATTTCACCAACTGTTGCTGGAAGATTCAAAACTGGAAGCAAAAACT 840

Qy        841 TGCTTGATTTTTTTTTCTTGTTAACGTAATAATAGAGACATTTTTAAAAGCACACAGCTC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TGCTTGATTTTTTTTTCTTGTTAACGTAATAATAGAGACATTTTTAAAAGCACACAGCTC 900

Qy        901 AAAGTCAGCCAATAAGTCTTTTCCTATTTGTGACTTTTACTAATAAAAATAAATCTGCCT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 AAAGTCAGCCAATAAGTCTTTTCCTATTTGTGACTTTTACTAATAAAAATAAATCTGCCT 960

Qy        961 GTAAATTATCTTGAAGTCCTTTACCTGGAACAAGCACTCTCTTTTTCACCACATAGTTTT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GTAAATTATCTTGAAGTCCTTTACCTGGAACAAGCACTCTCTTTTTCACCACATAGTTTT 1020

Qy       1021 AACTTGACTTTCAAGATAATTTTCAGGGTTTTTGTTGTTGTTGTTTTTTGTTTGTTTGTT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AACTTGACTTTCAAGATAATTTTCAGGGTTTTTGTTGTTGTTGTTTTTTGTTTGTTTGTT 1080

Qy       1081 TTGGTGGGAGAGGGGAGGGATGCCTGGGAAGTGGTTAACAACTTTTTTCAAGTCACTTTA 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TTGGTGGGAGAGGGGAGGGATGCCTGGGAAGTGGTTAACAACTTTTTTCAAGTCACTTTA 1140

Qy       1141 CTAAACAAACTTTTGTAAATAGACCTTACCTTCTATTTTCGAGTTTCATTTATATTTTGC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 CTAAACAAACTTTTGTAAATAGACCTTACCTTCTATTTTCGAGTTTCATTTATATTTTGC 1200

Qy       1201 AGTGTAGCCAGCCTCATCAAAGAGCTGACTTACTCATTTGACTTTTGCACTGACTGTATT 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AGTGTAGCCAGCCTCATCAAAGAGCTGACTTACTCATTTGACTTTTGCACTGACTGTATT 1260

Qy       1261 ATCTGGGTATCTGCTGTGTCTGCACTTCATGGTAAACGGGATCTAAAATGCCTGGTGGCT 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 ATCTGGGTATCTGCTGTGTCTGCACTTCATGGTAAACGGGATCTAAAATGCCTGGTGGCT 1320

Qy       1321 TTTCACAAAAAGCAGATTTTCTTCATGTACTGTGATGTCTGATGCAATGCATCCTAGAAC 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 TTTCACAAAAAGCAGATTTTCTTCATGTACTGTGATGTCTGATGCAATGCATCCTAGAAC 1380

Qy       1381 AAACTGGCCATTTGCTAGTTTACTCTAAAGACTAAACATAGTCTTGGTGTGTGTGGTCTT 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 AAACTGGCCATTTGCTAGTTTACTCTAAAGACTAAACATAGTCTTGGTGTGTGTGGTCTT 1440

Qy       1441 ACTCATCTTCTAGTACCTTTAAGGACAAATCCTAAGGACTTGGACACTTGCAATAAAGAA 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 ACTCATCTTCTAGTACCTTTAAGGACAAATCCTAAGGACTTGGACACTTGCAATAAAGAA 1500

Qy       1501 ATTTTATTTTAAACCCAAGCCTCCCTGGATTGATAATATATACACATTTGTCAGCATTTC 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       1501 ATTTTATTTTAAACCCAAGCCTCCCTGGATTGATAATATATACACATTTGTCAGCATTTC 1560

Qy       1561 CGGTCGTGGTGAGAGGCAGCTGTTTGAGCTCCAATATGTGCAGCTTTGAACTAGGGCTGG 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 CGGTCGTGGTGAGAGGCAGCTGTTTGAGCTCCAATATGTGCAGCTTTGAACTAGGGCTGG 1620

Qy       1621 GGTTGTGGGTGCCTCTTCTGAAAGGTCTAACCATTATTGGATAACTGGCTTTTTTCTTCC 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 GGTTGTGGGTGCCTCTTCTGAAAGGTCTAACCATTATTGGATAACTGGCTTTTTTCTTCC 1680

Qy       1681 TATGTCCTCTTTGGAATGTAACAATAAAAATAATTTTTGAAACATCAA 1728
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 TATGTCCTCTTTGGAATGTAACAATAAAAATAATTTTTGAAACATCAA 1728
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RESULT 11
ACA64436
ID ACA64436 standard; cDNA; 1728 BP.
XX
AC ACA64436;
XX
DT 17-JUN-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO1375 cDNA.
XX
KW Human; secreted and transmembrane protein; cytostatic; anti-HIV;
KW virucide; hepatotropic; antiinflammatory; neuroprotective; gene therapy;
KW PRO; pharmaceutical; diagnostic; biosensor; bioreactor; malignancy;
KW cancer; ovarian cancer; colorectal cancer; Kaposi's sarcoma; leukaemia;
KW lymphoma; hepatitis B; multiple sclerosis; Crohn's disease;
KW drug screening; gene; ss.
XX
OS Homo sapiens.
XX
PN US2003003531-A1.
XX
PD 02-JAN-2003.
XX
PF 19-NOV-2001; 2001US-00989734.
XX
PR 16-JUN-1997; 97US-0049787P.
PR 17-OCT-1997; 97US-0062250P.
PR 05-NOV-1997; 97WO-US020069.
PR 12-NOV-1997; 97US-0065186P.
PR 13-NOV-1997; 97US-0065311P.
PR 24-NOV-1997; 97US-0066770P.
PR 25-FEB-1998; 98US-0075945P.
PR 20-MAR-1998; 98US-0078910P.
PR 28-APR-1998; 98US-0083322P.
PR 07-MAY-1998; 98US-0084600P.
PR 28-MAY-1998; 98US-0087106P.
PR 02-JUN-1998; 98US-0087607P.
PR 02-JUN-1998; 98US-0087609P.
PR 02-JUN-1998; 98US-0087759P.
PR 03-JUN-1998; 98US-0087827P.
PR 04-JUN-1998; 98US-0088021P.
PR 04-JUN-1998; 98US-0088025P.
PR 04-JUN-1998; 98US-0088026P.
PR 04-JUN-1998; 98US-0088028P.
PR 04-JUN-1998; 98US-0088029P.
PR 04-JUN-1998; 98US-0088030P.
PR 04-JUN-1998; 98US-0088033P.
PR 04-JUN-1998; 98US-0088326P.
PR 05-JUN-1998; 98US-0088167P.
PR 05-JUN-1998; 98US-0088202P.
PR 05-JUN-1998; 98US-0088212P.
PR 05-JUN-1998; 98US-0088217P.
PR 09-JUN-1998; 98US-0088655P.
PR 10-JUN-1998; 98US-0088734P.
PR 10-JUN-1998; 98US-0088738P.
PR 10-JUN-1998; 98US-0088742P.
PR 10-JUN-1998; 98US-0088810P.
PR 10-JUN-1998; 98US-0088824P.

PR 10-JUN-1998; 98US-0088826P.
PR 11-JUN-1998; 98US-0088858P.
PR 11-JUN-1998; 98US-0088861P.
PR 11-JUN-1998; 98US-0088876P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089440P.
PR 16-JUN-1998; 98US-0089512P.
PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089532P.
PR 17-JUN-1998; 98US-0089538P.
PR 17-JUN-1998; 98US-0089598P.
PR 17-JUN-1998; 98US-0089599P.
PR 17-JUN-1998; 98US-0089600P.
PR 17-JUN-1998; 98US-0089653P.
PR 18-JUN-1998; 98US-0089801P.
PR 18-JUN-1998; 98US-0089907P.
PR 18-JUN-1998; 98US-0089908P.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 02-JUN-1999; 99WO-US012252.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 28-AUG-2001; 2001US-00941992.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
PI Zhang Z;
XX
DR WPI; 2003-352829/33.
DR P-PSDB; ABU72576.
XX
PT New genes and secreted and transmembrane polypeptides (e.g. PRO183 or
PT PRO184), useful for treating or diagnosing e.g. ovarian cancer, Kaposi's
PT sarcoma, leukemia, lymphoma, hepatitis B, multiple sclerosis or Crohn's
PT disease.
XX
PS Claim 1; Fig 299; 663pp; English.
XX
CC The invention describes a new isolated nucleic acid molecule comprising
CC the full length coding sequence of the DNA deposited with the American
CC Type Culture Collection (e.g. ATCC Deposit No. 209621, 552-PTA, 819-PTA,
CC 209439, 203135, etc); or a sequence with at least 80% identity to a DNA
CC encoding a PRO polypeptide. The PRO polypeptides or polynucleotides are
CC useful as pharmaceuticals, diagnostics, biosensors or bioreactors. These
CC are particularly useful for detecting or treating e.g. malignancies or
CC cancers (e.g. ovarian cancer, colorectal cancer, Kaposi's sarcoma,
CC leukaemia or lymphoma), hepatitis B, multiple sclerosis, or Crohn's
CC disease in mammals. The PRO polypeptides are useful in drug screening,
CC particularly as targets for therapeutic intervention in these diseases,
CC and in the diagnostic determination of the presence of these diseases.
CC The PRO polypeptides are also useful as molecular weight markers, or for
CC chromosome identification. The PRO genes are useful as hybridisation
CC probes, or for screening libraries of human cDNA, genomic DNA or mRNA.
CC The PRO genes may also be used in gene therapy, particularly for
CC replacing a defective gene. This sequence encodes a novel human secreted
CC and transmembrane PRO polypeptide
XX
SQ Sequence 1728 BP; 438 A; 360 C; 390 G; 540 T; 0 U; 0 Other;

Query Match 100.0%; Score 1728; DB 7; Length 1728;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1728; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          1 CAGCCGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCC 60

Qy         61 GGTCGCGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCCAGCGATGGCGACCCTGTGGGG 120
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Db         61 GGTCGCGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCCAGCGATGGCGACCCTGTGGGG 120

Qy        121 AGGCCTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTTCCGTGCTGCT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AGGCCTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTTCCGTGCTGCT 180

Qy        181 GCTGGCGCAGCTGTCAGACGCCGCCAAGAATTTCGAGGATGTCAGATGTAAATGTATCTG 240
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Db        181 GCTGGCGCAGCTGTCAGACGCCGCCAAGAATTTCGAGGATGTCAGATGTAAATGTATCTG 240

Qy        241 CCCTCCCTATAAAGAAAATTCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CCCTCCCTATAAAGAAAATTCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTG 300

Qy        301 TGATTGCCTTCATGTTGTGGAGCCCATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGATTGCCTTCATGTTGTGGAGCCCATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTG 360

Qy        361 TCTACGCTGTGAATGCAAATATGAAGAAAGAAGCTCTGTCACAATCAAGGTTACCATTAT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TCTACGCTGTGAATGCAAATATGAAGAAAGAAGCTCTGTCACAATCAAGGTTACCATTAT 420

Qy        421 AATTTATCTCTCCATTTTGGGCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGA 480
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Db        421 AATTTATCTCTCCATTTTGGGCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGA 480

Qy        481 GCCCATACTGAAGAGGCGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATAT 540
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Db        481 GCCCATACTGAAGAGGCGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATAT 540

Qy        541 TGGGGATCACCAGCCTTTTGCAAATGCACACGATGTGCTAGCCCGCTCCCGCAGTCGAGC 600
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Db        541 TGGGGATCACCAGCCTTTTGCAAATGCACACGATGTGCTAGCCCGCTCCCGCAGTCGAGC 600

Qy        601 CAACGTGCTGAACAAGGTAGAATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCA 660
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Db        601 CAACGTGCTGAACAAGGTAGAATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCA 660

Qy        661 GCGAAAGTCTGTCTTTGACCGGCATGTTGTCCTCAGCTAATTGGGAATTGAATTCAAGGT 720
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Qy        721 GACTAGAAAGAAACAGGCAGACAACTGGAAAGAACTGACTGGGTTTTGCTGGGTTTCATT 780
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Qy        781 TTAATACCTTGTTGATTTCACCAACTGTTGCTGGAAGATTCAAAACTGGAAGCAAAAACT 840
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Db        781 TTAATACCTTGTTGATTTCACCAACTGTTGCTGGAAGATTCAAAACTGGAAGCAAAAACT 840

Qy        841 TGCTTGATTTTTTTTTTCTTGTTAACGTAATAATAGAGACATTTTTAAAAGCACACAGCTC 900
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Db        841 TGCTTGATTTTTTTTTTCTTGTTAACGTAATAATAGAGACATTTTTAAAAGCACACAGCTC 900

Qy        901 AAAGTCAGCCAATAAGTCTTTTCCTATTTGTGACTTTTACTAATAAAAATAAATCTGCCT 960
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Db        901 AAAGTCAGCCAATAAGTCTTTTCCTATTTGTGACTTTTACTAATAAAAATAAATCTGCCT 960

Qy        961 GTAAATTATCTTGAAGTCCTTTACCTGGAACAAGCACTCTCTTTTTTCACCACATAGTTTT 1020
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Db        961 GTAAATTATCTTGAAGTCCTTTACCTGGAACAAGCACTCTCTTTTTCACCACATAGTTTT 1020

Qy       1021 AACTTGACTTTCAAGATAATTTTCAGGGTTTTTGTTGTTGTTGTTTTTTGTTTGTTTGTT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AACTTGACTTTCAAGATAATTTTCAGGGTTTTTGTTGTTGTTGTTTTTTGTTTGTTTGTT 1080

Qy       1081 TTGGTGGGAGAGGGGAGGGATGCCTGGGAAGTGGTTAACAACTTTTTTCAAGTCACTTTA 1140
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Db       1081 TTGGTGGGAGAGGGGAGGGATGCCTGGGAAGTGGTTAACAACTTTTTTCAAGTCACTTTA 1140

Qy       1141 CTAAACAAACTTTTGTAAATAGACCTTACCTTCTATTTTCGAGTTTCATTTATATTTTGC 1200
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Db       1141 CTAAACAAACTTTTGTAAATAGACCTTACCTTCTATTTTCGAGTTTCATTTATATTTTGC 1200

Qy       1201 AGTGTAGCCAGCCTCATCAAAGAGCTGACTTACTCATTTGACTTTTGCACTGACTGTATT 1260
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Db       1201 AGTGTAGCCAGCCTCATCAAAGAGCTGACTTACTCATTTGACTTTTGCACTGACTGTATT 1260

Qy       1261 ATCTGGGTATCTGCTGTGTCTGCACTTCATGGTAAACGGGATCTAAAATGCCTGGTGGCT 1320
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Db       1261 ATCTGGGTATCTGCTGTGTCTGCACTTCATGGTAAACGGGATCTAAAATGCCTGGTGGCT 1320

Qy       1321 TTTCACAAAAAGCAGATTTTCTTCATGTACTGTGATGTCTGATGCAATGCATCCTAGAAC 1380
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Db       1321 TTTCACAAAAAGCAGATTTTCTTCATGTACTGTGATGTCTGATGCAATGCATCCTAGAAC 1380

Qy       1381 AAACTGGCCATTTGCTAGTTTACTCTAAAGACTAAACATAGTCTTGGTGTGTGTGGTCTT 1440
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RESULT 12
ACA58005
ID   ACA58005 standard; cDNA; 1728 BP.
XX
AC   ACA58005;
XX
DT   09-JUN-2003  (first entry)
XX
DE   cDNA encoding human neoplasia inhibiting PRO polypeptide PRO1375.
XX
KW   Human; ss; gene; tumour; cancer; neoplasia; liver cancer; sarcoma;
KW   breast cancer; ovarian cancer; renal cancer; colorectal cancer; melanoma;
KW   uterine cancer; prostate cancer; lung cancer; bladder cancer; leukaemia;
KW   gastric cancer; pancreatic cancer; vulval cancer; thyroid cancer;
KW   central nervous system cancer; hepatic carcinoma; glioblastoma;
KW   neuronal disorder; glial disorder; astrocytal disorder;
KW   hypothalamic disorder; glandular disorder; macrophagal disorder;
KW   epithelial disorder; stromal disorder; blastocoelic disorder;
KW   inflammatory disorder; angiogenic disorder; immunologic disorder.
XX
OS   Homo sapiens.
XX
PN   US2002192209-A1.
XX
PD   19-DEC-2002.
XX
PF   30-NOV-2001; 2001US-00001054.
XX
PR   17-SEP-1997;   97US-0059114P.
PR   27-MAR-1998;   98US-0079689P.
PR   30-MAR-1998;   98US-0079920P.
PR   24-APR-1998;   98US-0082999P.
PR   29-APR-1998;   98US-0083545P.
PR   12-MAY-1998;   98US-0085149P.
PR   02-JUN-1998;   98US-0087607P.
PR   11-JUN-1998;   98US-0088858P.
PR   25-JUN-1998;   98US-0090691P.
PR   17-AUG-1998;   98US-0096891P.
PR   17-AUG-1998;   98US-0096894P.
PR   10-SEP-1998;   98US-0099803P.
PR   10-SEP-1998;   98WO-US018824.
PR   14-SEP-1998;   98US-0100263P.
PR   15-SEP-1998;   98US-0100390P.
PR   23-SEP-1998;   98US-0101476P.
PR   10-NOV-1998;   98US-0107783P.
PR   18-NOV-1998;   98US-0108849P.
PR   19-NOV-1998;   98US-00180997.
PR   15-DEC-1998;   98US-0112420P.
PR   22-DEC-1998;   98US-00218517.
PR   22-DEC-1998;   98US-0113296P.
PR   05-JAN-1999;   99WO-US000106.
PR   12-JAN-1999;   99US-0115554P.
PR   12-JAN-1999;   99US-0115558P.
PR   20-JAN-1999;   99US-0116533P.
PR   08-MAR-1999;   99WO-US005028.
PR   10-MAR-1999;   99US-0123618P.
PR   12-APR-1999;   99US-00284291.
PR   20-APR-1999;   99WO-US008615.
PR   27-APR-1999;   99US-0131294P.
PR   02-JUN-1999;   99WO-US012252.
PR   22-JUN-1999;   99US-0140650P.
PR   23-JUN-1999;   99US-0141037P.
PR   20-JUL-1999;   99US-0144758P.
PR   25-AUG-1999;   99US-00380137.
PR   25-AUG-1999;   99US-00380138.
PR   01-SEP-1999;   99WO-US020111.
PR   08-SEP-1999;   99WO-US020594.
PR   09-SEP-1999;   99US-00380913.
PR   18-OCT-1999;   99US-00403297.
PR   29-OCT-1999;   99US-0162506P.
PR   10-NOV-1999;   99US-00423741.
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PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 09-DEC-1999; 99US-0170262P.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030999.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 02-MAR-2000; 2000WO-US005841.
PR 03-MAR-2000; 2000US-0187202P.
PR 15-MAR-2000; 2000WO-US006884.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 08-NOV-2000; 2000US-00709238.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872034.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 14-JUN-2001; 2001US-00882636.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 30-JUL-2001; 2001US-00918585.
PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.
PR 13-AUG-2001; 2001US-00929404.
PR 28-AUG-2001; 2001US-00941992.
PR 29-AUG-2001; 2001WO-US027099.
PR 04-SEP-2001; 2001US-00946374.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W, Kabakoff RC;
PI Shelton DL, Smith V, Watanabe CK, Wood WI;
XX
DR WPI; 2003-328851/06.
DR P-PSDB; ABU71431.
XX
PT Novel isolated PRO polypeptides e.g. PRO240, PRO381, PRO540, useful for
PT treating tumor, preferably cancer, or for treating neuronal, glial,
PT hypothalamic, stromal, inflammatory, angiogenic and immunologic
PT disorders.
XX
PS Claim 20; Fig 31; 186pp; English.
XX
CC The invention relates to an isolated secreted and transmembrane
CC polypeptide, designated as PRO polypeptide, PRO polypeptide lacking its
CC associated signal peptide or PRO polypeptide extracellular domain with or
CC without its associated signal peptide. The PRO polypeptide or an antibody
CC binding to it is useful for inhibiting the growth of a tumor cell. A
CC composition containing a PRO polypeptide is useful for inhibiting
CC neoplastic cell growth or for treating a tumour, preferably cancer (such
CC as liver, breast, ovarian, renal, colorectal, uterine, prostate, lung,
CC bladder, gastric, pancreatic, vulval, thyroid, central nervous system
CC cancer, hepatic carcinomas, sarcomas, glioblastomas, melanoma or
CC leukaemia) in a mammal. The PRO polypeptide is useful for identifying its
CC agonists. The PRO polypeptide or an antibody binding to it is useful in
CC the preparation of a medicament for treating a condition which is
CC responsive to the PRO polypeptide or an antibody binding to it. The PRO
CC polypeptide or an antibody binding to it is also useful for treating
CC neuronal, glial, astrocytal, hypothalamic, glandular, macrophagal,
CC epithelial, stromal, blastocoelic, inflammatory, angiogenic and
CC immunologic disorders. The present sequence represents a cDNA encoding a
CC PRO polypeptides of the invention
XX
SQ Sequence 1728 BP; 438 A; 360 C; 390 G; 540 T; 0 U; 0 Other;

Query Match 100.0%; Score 1728; DB 7; Length 1728;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1728; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 CAGCCGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCC 60
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Qy         61 GGTCGCGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCCAGCGATGGCGACCCTGTGGGG 120
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RESULT 13
ABX80895
ID   ABX80895 standard; cDNA; 1728 BP.
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AC   ABX80895;
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DT   22-APR-2003  (first entry)
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DE   Human secreted/transmembrane protein cDNA, #168.
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KW   Human; gene; ss; PRO; secreted; transmembrane; pharmaceutical;
KW   diagnostic; biosensor; bioreactor; tumour; therapeutic; gene therapy;
KW   tumour-associated antigenic target; TAT; ADEPT;
KW   antibody-dependent enzyme mediated prodrug therapy; cytostatic.
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OS   Homo sapiens.
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PN   US2003027162-A1.
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PD   06-FEB-2003.
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PF   15-NOV-2001; 2001US-00997428.
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Query Match 100.0%; Score 1728; DB 7; Length 1728;
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Qy       1021 AACTTGACTTTCAAGATAATTTTCAGGGTTTTTGTTGTTGTTGTTTTTTTGTTTGTTTGTT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AACTTGACTTTCAAGATAATTTTCAGGGTTTTTGTTGTTGTTGTTTTTTTGTTTGTTTGTT 1080

Qy       1081 TTGGTGGGAGAGGGGAGGGATGCCTGGGAAGTGGTTAACAACTTTTTTCAAGTCACTTTA 1140
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Db       1081 TTGGTGGGAGAGGGGAGGGATGCCTGGGAAGTGGTTAACAACTTTTTTCAAGTCACTTTA 1140

Qy       1141 CTAAACAAACTTTTGTAAATAGACCTTACCTTCTATTTTCGAGTTTCATTTATATTTTGC 1200
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Db       1141 CTAAACAAACTTTTGTAAATAGACCTTACCTTCTATTTTCGAGTTTCATTTATATTTTGC 1200

Qy       1201 AGTGTAGCCAGCCTCATCAAAGAGCTGACTTACTCATTTGACTTTTGCACTGACTGTATT 1260
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Db       1201 AGTGTAGCCAGCCTCATCAAAGAGCTGACTTACTCATTTGACTTTTGCACTGACTGTATT 1260

Qy       1261 ATCTGGGTATCTGCTGTGTCTGCACTTCATGGTAAACGGGATCTAAAATGCCTGGTGGCT 1320
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Db       1261 ATCTGGGTATCTGCTGTGTCTGCACTTCATGGTAAACGGGATCTAAAATGCCTGGTGGCT 1320

Qy       1321 TTTCACAAAAAGCAGATTTTCTTCATGTACTGTGATGTCTGATGCAATGCATCCTAGAAC 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 TTTCACAAAAAGCAGATTTTCTTCATGTACTGTGATGTCTGATGCAATGCATCCTAGAAC 1380

Qy       1381 AAACTGGCCATTTGCTAGTTTACTCTAAAGACTAAACATAGTCTTGGTGTGTGTGGTCTT 1440
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Db       1381 AAACTGGCCATTTGCTAGTTTACTCTAAAGACTAAACATAGTCTTGGTGTGTGTGGTCTT 1440

Qy       1441 ACTCATCTTCTAGTACCTTTAAGGACAAATCCTAAGGACTTGGACACTTGCAATAAAGAA 1500
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Db       1441 ACTCATCTTCTAGTACCTTTAAGGACAAATCCTAAGGACTTGGACACTTGCAATAAAGAA 1500

Qy       1501 ATTTTATTTTAAACCCAAGCCTCCCTGGATTGATAATATATACACATTTGTCAGCATTTC 1560
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Db       1501 ATTTTATTTTAAACCCAAGCCTCCCTGGATTGATAATATATACACATTTGTCAGCATTTC 1560

Qy       1561 CGGTCGTGGTGAGAGGCAGCTGTTTGAGCTCCAATATGTGCAGCTTTGAACTAGGGCTGG 1620
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Db       1561 CGGTCGTGGTGAGAGGCAGCTGTTTGAGCTCCAATATGTGCAGCTTTGAACTAGGGCTGG 1620

Qy       1621 GGTTGTGGGTGCCTCTTCTGAAAGGTCTAACCATTATTGGATAACTGGCTTTTTTCTTCC 1680
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Db       1621 GGTTGTGGGTGCCTCTTCTGAAAGGTCTAACCATTATTGGATAACTGGCTTTTTTCTTCC 1680

Qy       1681 TATGTCCTCTTTGGAATGTAACAATAAAAATAATTTTTGAAACATCAA 1728
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Db       1681 TATGTCCTCTTTGGAATGTAACAATAAAAATAATTTTTGAAACATCAA 1728
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RESULT 14
ACD44404
ID ACD44404 standard; cDNA; 1728 BP.
XX
AC ACD44404;
XX
DT 10-SEP-2003 (first entry)
XX
DE cDNA encoding human PRO1375 polypeptide.
XX
KW Human; PRO polypeptide; secreted protein; transmembrane protein;
KW genetic disorder; antibacterial; immunosuppressive; transgenic;
KW gene therapy; gene; ss.
XX
OS Homo sapiens.
XX
PN US2002127576-A1.
XX
PD 12-SEP-2002.
XX
PF 14-NOV-2001; 2001US-00991073.
XX
PR 16-JUN-1997; 97US-0049787P.
PR 17-OCT-1997; 97US-0062250P.
PR 05-NOV-1997; 97WO-US020069.
PR 12-NOV-1997; 97US-0065186P.
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PR 24-NOV-1997; 97US-0066770P.
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PR 28-APR-1998; 98US-0083322P.
PR 07-MAY-1998; 98US-0084600P.
PR 28-MAY-1998; 98US-0087106P.
PR 02-JUN-1998; 98US-0087607P.
PR 02-JUN-1998; 98US-0087609P.
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PR 03-JUN-1998; 98US-0087827P.
PR 04-JUN-1998; 98US-0088021P.
PR 04-JUN-1998; 98US-0088025P.
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PR 11-JUN-1998; 98US-0088876P.

PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089440P.
PR 16-JUN-1998; 98US-0089512P.
PR 16-JUN-1998; 98US-0089514P.
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PR 17-JUN-1998; 98US-0089599P.
PR 17-JUN-1998; 98US-0089600P.
PR 17-JUN-1998; 98US-0089653P.
PR 18-JUN-1998; 98US-0089801P.
PR 18-JUN-1998; 98US-0089907P.
PR 18-JUN-1998; 98US-0089908P.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 02-JUN-1999; 99WO-US012252.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 06-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 28-AUG-2001; 2001US-00941992.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
PI Zhang Z;
XX
DR WPI; 2003-340824/32.
DR P-PSDB; ABO26022.
XX
PT Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346
PT and PRO1375, which stimulate proliferation of stimulated T-lymphocytes
PT and are therapeutically useful for enhancing immune responses.
XX
PS Claim 2; Fig 299; 661pp; English.

XX
CC The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The PRO
CC polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides are useful for detecting other PRO polypeptides, for linking
CC bioactive molecules to cells expressing PRO polypeptides, for modulating
CC biological activities of cells expressing PRO polypeptides, and for for
CC identifying agonists or antagonists. The polynucleotide sequences
CC encoding PRO polypeptides are useful as hybridisation probes, in
CC chromosome and gene mapping, in the generation of antisense RNA and DNA,
CC in the preparation of PRO polypeptides, for generating transgenic animals
CC or knockout animals, to construct hybridisation probes for mapping the
CC gene which encodes the PRO polypeptide, and for the genetic analysis of
CC individuals with genetic disorders, in gene therapy, for chromosome
CC identification, as chromosome markers, and for generating probes for PCR,
CC Northern analysis, Southern analysis and Western analysis. The present
CC sequence encodes a human PRO polypeptide of the invention. Note: The
CC sequence data for this patent was obtained in electronic format directly
CC from the USPTO web site at seqdata.uspto.gov/psipsDIDEntry.html
XX
SQ Sequence 1728 BP; 438 A; 360 C; 390 G; 540 T; 0 U; 0 Other;

Query Match 100.0%; Score 1728; DB 7; Length 1728;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1728; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    1 CAGCCGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCC 60
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Db    1 CAGCCGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCC 60

Qy   61 GGTCGCGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCCAGCGATGGCGACCCTGTGGGG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GGTCGCGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCCAGCGATGGCGACCCTGTGGGG 120

Qy  121 AGGCCTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTTCCGTGCTGCT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 AGGCCTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTTCCGTGCTGCT 180

Qy  181 GCTGGCGCAGCTGTCAGACGCCGCCAAGAATTTCGAGGATGTCAGATGTAAATGTATCTG 240
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Db  181 GCTGGCGCAGCTGTCAGACGCCGCCAAGAATTTCGAGGATGTCAGATGTAAATGTATCTG 240

Qy  241 CCCTCCCTATAAAGAAAATTCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTG 300
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Db  241 CCCTCCCTATAAAGAAAATTCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTG 300

Qy  301 TGATTGCCTTCATGTTGTGGAGCCCATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTG 360
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Db  301 TGATTGCCTTCATGTTGTGGAGCCCATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTG 360

Qy  361 TCTACGCTGTGAATGCAAATATGAAGAAAGAAGCTCTGTCACAATCAAGGTTACCATTAT 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 TCTACGCTGTGAATGCAAATATGAAGAAAGAAGCTCTGTCACAATCAAGGTTACCATTAT 420

Qy  421 AATTTATCTCTCCATTTTGGGCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 AATTTATCTCTCCATTTTGGGCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGA 480

Qy  481 GCCCATACTGAAGAGGCGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATAT 540
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Db  481 GCCCATACTGAAGAGGCGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATAT 540

Qy  541 TGGGGATCACCAGCCTTTTGCAAATGCACACGATGTGCTAGCCCGCTCCCGCAGTCGAGC 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  541 TGGGGATCACCAGCCTTTTGCAAATGCACACGATGTGCTAGCCCGCTCCCGCAGTCGAGC 600

Qy  601 CAACGTGCTGAACAAGGTAGAATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCA 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  601 CAACGTGCTGAACAAGGTAGAATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCA 660

Qy  661 GCGAAAGTCTGTCTTTGACCGGCATGTTGTCCTCAGCTAATTGGGAATTGAATTCAAGGT 720
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Qy        721 GACTAGAAAGAAACAGGCAGACAACTGGAAAGAACTGACTGGGTTTTGCTGGGTTTCATT 780
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Db        721 GACTAGAAAGAAACAGGCAGACAACTGGAAAGAACTGACTGGGTTTTGCTGGGTTTCATT 780

Qy        781 TTAATACCTTGTTGATTTCACCAACTGTTGCTGGAAGATTCAAAACTGGAAGCAAAAACT 840
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Qy        841 TGCTTGATTTTTTTTTCTTGTTAACGTAATAATAGAGACATTTTTAAAAGCACACAGCTC 900
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Qy        901 AAAGTCAGCCAATAAGTCTTTTCCTATTTGTGACTTTTACTAATAAAAATAAATCTGCCT 960
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Db        901 AAAGTCAGCCAATAAGTCTTTTCCTATTTGTGACTTTTACTAATAAAAATAAATCTGCCT 960

Qy        961 GTAAATTATCTTGAAGTCCTTTACCTGGAACAAGCACTCTCTTTTTCACCACATAGTTTT 1020
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Db        961 GTAAATTATCTTGAAGTCCTTTACCTGGAACAAGCACTCTCTTTTTCACCACATAGTTTT 1020

Qy       1021 AACTTGACTTTCAAGATAATTTTCAGGGTTTTTGTTGTTGTTGTTTTTTGTTTGTTTGTT 1080
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Db       1021 AACTTGACTTTCAAGATAATTTTCAGGGTTTTTGTTGTTGTTGTTTTTTGTTTGTTTGTT 1080

Qy       1081 TTGGTGGGAGAGGGGAGGGATGCCTGGGAAGTGGTTAACAACTTTTTTCAAGTCACTTTA 1140
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Db       1081 TTGGTGGGAGAGGGGAGGGATGCCTGGGAAGTGGTTAACAACTTTTTTCAAGTCACTTTA 1140

Qy       1141 CTAAACAAACTTTTGTAAATAGACCTTACCTTCTATTTTCGAGTTTCATTTATATTTTGC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 CTAAACAAACTTTTGTAAATAGACCTTACCTTCTATTTTCGAGTTTCATTTATATTTTGC 1200

Qy       1201 AGTGTAGCCAGCCTCATCAAAGAGCTGACTTACTCATTTGACTTTTGCACTGACTGTATT 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AGTGTAGCCAGCCTCATCAAAGAGCTGACTTACTCATTTGACTTTTGCACTGACTGTATT 1260

Qy       1261 ATCTGGGTATCTGCTGTGTCTGCACTTCATGGTAAACGGGATCTAAAATGCCTGGTGGCT 1320
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Db       1261 ATCTGGGTATCTGCTGTGTCTGCACTTCATGGTAAACGGGATCTAAAATGCCTGGTGGCT 1320

Qy       1321 TTTCACAAAAAGCAGATTTTCTTCATGTACTGTGATGTCTGATGCAATGCATCCTAGAAC 1380
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Db       1321 TTTCACAAAAAGCAGATTTTCTTCATGTACTGTGATGTCTGATGCAATGCATCCTAGAAC 1380

Qy       1381 AAACTGGCCATTTGCTAGTTTACTCTAAAGACTAAACATAGTCTTGGTGTGTGTGGTCTT 1440
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Db       1381 AAACTGGCCATTTGCTAGTTTACTCTAAAGACTAAACATAGTCTTGGTGTGTGTGGTCTT 1440

Qy       1441 ACTCATCTTCTAGTACCTTTAAGGACAAATCCTAAGGACTTGGACACTTGCAATAAAGAA 1500
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Qy       1681 TATGTCCTCTTTGGAATGTAACAATAAAAATAATTTTTGAAACATCAA 1728
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RESULT 15
ABX79575
ID ABX79575 standard; cDNA; 1728 BP.

XX
AC ABX79575;
XX
DT 17-APR-2003 (first entry)
XX
DE Human sectreted/transmembrane protein cDNA, #168.
XX
KW Human; gene; ss; PRO; secreted; transmembrane; signal peptide;
KW pharmaceutical; diagnostic; biosensor; bioreactor; tumour; therapeutic;
KW colon cancer; lung cancer; breast cancer; cancer; gene therapy.
XX
OS Homo sapiens.
XX
PN US2002142961-A1.
XX
PD 03-OCT-2002.
XX
PF 19-NOV-2001; 2001US-00989721.
XX
PR 16-JUN-1997; 97US-0049787P.
PR 17-OCT-1997; 97US-0062250P.
PR 05-NOV-1997; 97WO-US020069.
PR 12-NOV-1997; 97US-0065186P.
PR 13-NOV-1997; 97US-0065311P.
PR 24-NOV-1997; 97US-0066770P.
PR 25-FEB-1998; 98US-0075945P.
PR 20-MAR-1998; 98US-0078910P.
PR 28-APR-1998; 98US-0083322P.
PR 07-MAY-1998; 98US-0084600P.
PR 28-MAY-1998; 98US-0087106P.
PR 02-JUN-1998; 98US-0087607P.
PR 02-JUN-1998; 98US-0087609P.
PR 02-JUN-1998; 98US-0087759P.
PR 03-JUN-1998; 98US-0087827P.
PR 04-JUN-1998; 98US-0088021P.
PR 04-JUN-1998; 98US-0088025P.
PR 04-JUN-1998; 98US-0088026P.
PR 04-JUN-1998; 98US-0088028P.
PR 04-JUN-1998; 98US-0088029P.
PR 04-JUN-1998; 98US-0088030P.
PR 04-JUN-1998; 98US-0088033P.
PR 04-JUN-1998; 98US-0088326P.
PR 05-JUN-1998; 98US-0088167P.
PR 05-JUN-1998; 98US-0088202P.
PR 05-JUN-1998; 98US-0088212P.
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PR 09-JUN-1998; 98US-0088655P.
PR 10-JUN-1998; 98US-0088734P.
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PR 10-JUN-1998; 98US-0088824P.
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PR 11-JUN-1998; 98US-0088858P.
PR 11-JUN-1998; 98US-0088861P.
PR 11-JUN-1998; 98US-0088876P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089440P.
PR 16-JUN-1998; 98US-0089512P.
PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089532P.
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PR 17-JUN-1998; 98US-0089598P.
PR 17-JUN-1998; 98US-0089599P.
PR 17-JUN-1998; 98US-0089600P.
PR 17-JUN-1998; 98US-0089653P.
PR 18-JUN-1998; 98US-0089801P.
PR 18-JUN-1998; 98US-0089907P.
PR 18-JUN-1998; 98US-0089908P.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 01-DEC-1998; 98WO-US025108.

PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 02-JUN-1999; 99WO-US012252.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 28-AUG-2001; 2001US-00941992.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
PI Zhang Z;
XX
DR WPI; 2003-155950/15.
DR P-PSDB; ABU59031.
XX
PT New secreted and transmembrane PRO polypeptides (e.g. PRO183, PRO184,
PT PRO361 or PRO846) useful as targets for therapeutic intervention in
PT cancers (e.g. lung or breast cancers), or for diagnosing these cancers.
XX
PS Claim 2; Fig 299; 647pp; English.
XX
CC The invention discloses isolated PRO secreted/transmembrane polypeptides
CC comprising a sequence without signal peptide and the nucleic acid
CC encoding them. The polypeptides can be used to raise antibodies that
CC specifically bind to the PRO polypeptide, for linking a bioactive
CC molecule to a cell expressing a PRO protein and for modulating at least
CC one biological activity of a cell. The PRO polypeptides or
CC polynucleotides are also useful as pharmaceuticals, diagnostics,
CC biosensors or bioreactors, for detecting or treating e.g. tumours in
CC mammals, e.g. humans, dogs, cats, cattle, horses, sheep, pigs, goats or
CC rabbits as targets for therapeutic intervention in certain cancers (e.g.
CC colon, lung or breast cancers) and diagnostic determination of the
CC presence of these cancers. The PRO polypeptides are also useful as
CC molecular weight markers or for chromosome identification. The PRO genes
CC are useful as hybridisation probes or for screening libraries of human
CC cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene
CC therapy, particularly for replacing a defective gene. The sequences
CC presented in ABX79290-ABX79675 are the genes encoding, the primers
CC amplifying and the probes detecting the PRO polynucleotides of the
CC invention. Note: The sequence data for this patent is also available in
CC electronic format from USPTO at seqdata.uspto.gov/sequence.html
XX
SQ Sequence 1728 BP; 438 A; 360 C; 390 G; 540 T; 0 U; 0 Other;

Query Match 100.0%; Score 1728; DB 7; Length 1728;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1728; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        121 AGGCCTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTTCCGTGCTGCT 180
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Qy        181 GCTGGCGCAGCTGTCAGACGCCGCCAAGAATTTCGAGGATGTCAGATGTAAATGTATCTG 240
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Db        181 GCTGGCGCAGCTGTCAGACGCCGCCAAGAATTTCGAGGATGTCAGATGTAAATGTATCTG 240

Qy        241 CCCTCCCTATAAAGAAAATTCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTG 300
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Qy        301 TGATTGCCTTCATGTTGTGGAGCCCATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTG 360
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Qy        421 AATTTATCTCTCCATTTTGGGCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGA 480
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Qy       1021 AACTTGACTTTCAAGATAATTTTCAGGGTTTTTGTTGTTGTTGTTTTTTGTTTGTTTGTT 1080
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Qy       1081 TTGGTGGGAGAGGGGAGGGATGCCTGGGAAGTGGTTAACAACTTTTTTCAAGTCACTTTA 1140
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Qy       1141 CTAAACAAACTTTTGTAAATAGACCTTACCTTCTATTTTCGAGTTTCATTTATATTTTGC 1200
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Qy       1201 AGTGTAGCCAGCCTCATCAAAGAGCTGACTTACTCATTTGACTTTTGCACTGACTGTATT 1260
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Job time : 699 secs

GenCore version 5.1.6

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Run on: April 20, 2004, 01:58:41 ; Search time 6718 Seconds
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Title: US-09-989-725-417
Perfect score: 1728
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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45		196.8	11.4	1499	6	BD093294	BD093294 Amyloid b

ALIGNMENTS

RESULT 1
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LOCUS AR252653 1728 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 417 from patent US 6478825.
ACCESSION AR252653
VERSION AR252653.1 GI:27300561
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 1728)
AUTHORS Winterbottom,J.M., Shimp,L., Boyce,T.M. and Kaes,D.
TITLE Implant, method of making same and use of the implant for the treatment of bone defects
JOURNAL Patent: US 6478825-A 417 12-NOV-2002;

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ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1728;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CAGCCGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCC 60
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Qy         61 GGTCGCGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCCAGCGATGGCGACCCTGTGGGG 120
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Qy       1021 AACTTGACTTTCAAGATAATTTTCAGGGTTTTTGTTGTTGTTGTTTTTTGTTTGTTTGTT 1080
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Qy       1201 AGTGTAGCCAGCCTCATCAAAGAGCTGACTTACTCATTTGACTTTTGCACTGACTGTATT 1260
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Db       1201 AGTGTAGCCAGCCTCATCAAAGAGCTGACTTACTCATTTGACTTTTGCACTGACTGTATT 1260

Qy       1261 ATCTGGGTATCTGCTGTGTCTGCACTTCATGGTAAACGGGATCTAAAATGCCTGGTGGCT 1320
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Qy       1321 TTTCACAAAAAGCAGATTTTCTTCATGTACTGTGATGTCTGATGCAATGCATCCTAGAAC 1380
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Qy       1381 AAACTGGCCATTTGCTAGTTTACTCTAAAGACTAAACATAGTCTTGGTGTGTGTGGTCTT 1440
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Qy       1501 ATTTTATTTTAAACCCAAGCCTCCCTGGATTGATAATATATACACATTTGTCAGCATTTC 1560
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Qy       1681 TATGTCCTCTTTGGAATGTAACAATAAAAATAATTTTTGAAACATCAA 1728
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Db       1681 TATGTCCTCTTTGGAATGTAACAATAAAAATAATTTTTGAAACATCAA 1728

RESULT 2
AX055468
LOCUS       AX055468               1728 bp    DNA     linear   PAT 13-JAN-2001
DEFINITION  Sequence 98 from Patent WO0073452.
ACCESSION   AX055468
VERSION     AX055468.1  GI:12228731
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Ashkenazi,A.J., Baker,K.P., Chan,B., Goddard,A., Godowski,P.J.,
            Gurney,A.L., Hebert,C., Henzel,W., Kabakoff,R.C., Shelton,D.L.,
            Tumas,D., Watanabe,C.K. and Wood,W.I.
  TITLE     Compositions and methods for the treatment of immune related
            diseases
  JOURNAL   Patent: WO 0073452-A 98 07-DEC-2000;
            Genentech, Inc. (US)
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FEATURES             Location/Qualifiers
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             100.0%;  Score 1728;  DB 6;  Length 1728;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1728;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CAGCCGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CAGCCGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCC 60

Qy         61 GGTCGCGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCCAGCGATGGCGACCCTGTGGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGTCGCGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCCAGCGATGGCGACCCTGTGGGG 120

Qy        121 AGGCCTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTTCCGTGCTGCT 180
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Db        121 AGGCCTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTTCCGTGCTGCT 180

Qy        181 GCTGGCGCAGCTGTCAGACGCCGCCAAGAATTTCGAGGATGTCAGATGTAAATGTATCTG 240
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Qy        301 TGATTGCCTTCATGTTGTGGAGCCCATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTG 360
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Qy        361 TCTACGCTGTGAATGCAAATATGAAGAAAGAAGCTCTGTCACAATCAAGGTTACCATTAT 420
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RESULT 3
AX055716
LOCUS       AX055716                1728 bp    DNA     linear   PAT 13-JAN-2001
DEFINITION  Sequence 31 from Patent WO0073348.
ACCESSION   AX055716
VERSION     AX055716.1  GI:12228841
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Baker,K.P., Goddard,A., Gurney,A.L., Hebert,C., Henzel,W.,
            Kabakoff,R.C., Shelton,D.L., Smith,V., Watanabe,C.K. and Wood,W.I.
  TITLE     Methods and compositions for inhibiting neoplastic cell growth
  JOURNAL   Patent: WO 0073348-A 31 07-DEC-2000;
            Genentech, Inc. (US)
FEATURES             Location/Qualifiers
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ORIGIN

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  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1728;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy        961 GTAAATTATCTTGAAGTCCTTTACCTGGAACAAGCACTCTCTTTTTCACCACATAGTTTT 1020
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Db       1681 TATGTCCTCTTTGGAATGTAACAATAAAAATAATTTTTGAAACATCAA 1728


RESULT 4
AX077037
LOCUS       AX077037               1728 bp    DNA     linear   PAT 22-FEB-2001
DEFINITION  Sequence 25 from Patent WO0105972.
ACCESSION   AX077037
VERSION     AX077037.1  GI:13121664
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Ashkenazi,A.J., Baker,K.P., Fong,S., Goddard,A., Godowski,P.J.,
            Gurney,A.L., Hillan,K.J., Mark,M.R., Marsters,S.A., Pitti,R.M.,
            Tumas,D., Watanabe,C.K. and Wood,W.I.
  TITLE     Compositions and methods for the treatment of immune related
            diseases
  JOURNAL   Patent: WO 0105972-A 25 25-JAN-2001;
            Genentech, Inc. (US)
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  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1728;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy         61 GGTCGCGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCCAGCGATGGCGACCCTGTGGGG  120
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Qy        121 AGGCCTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTTCCGTGCTGCT  180
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Db        121 AGGCCTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTTCCGTGCTGCT  180

Qy        181 GCTGGCGCAGCTGTCAGACGCCGCCAAGAATTTCGAGGATGTCAGATGTAAATGTATCTG  240
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Db        181 GCTGGCGCAGCTGTCAGACGCCGCCAAGAATTTCGAGGATGTCAGATGTAAATGTATCTG  240

Qy        241 CCCTCCCTATAAAGAAAATTCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTG  300
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Db        241 CCCTCCCTATAAAGAAAATTCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTG  300

Qy        301 TGATTGCCTTCATGTTGTGGAGCCCATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTG  360
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Db        301 TGATTGCCTTCATGTTGTGGAGCCCATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTG  360

Qy        361 TCTACGCTGTGAATGCAAATATGAAGAAAGAAGCTCTGTCACAATCAAGGTTACCATTAT  420
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Qy        421 AATTTATCTCTCCATTTTGGGCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGA  480
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Qy        481 GCCCATACTGAAGAGGCGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATAT  540
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Qy        661 GCGAAAGTCTGTCTTTGACCGGCATGTTGTCCTCAGCTAATTGGGAATTGAATTCAAGGT  720
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Qy        721 GACTAGAAAGAAACAGGCAGACAACTGGAAAGAACTGACTGGGTTTTGCTGGGTTTCATT  780
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Qy        781 TTAATACCTTGTTGATTTCACCAACTGTTGCTGGAAGATTCAAAACTGGAAGCAAAAACT  840
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Qy       1261 ATCTGGGTATCTGCTGTGTCTGCACTTCATGGTAAACGGGATCTAAAATGCCTGGTGGCT  1320
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Qy       1381 AAACTGGCCATTTGCTAGTTTACTCTAAAGACTAAACATAGTCTTGGTGTGTGTGGTCTT  1440
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Qy       1441 ACTCATCTTCTAGTACCTTTAAGGACAAATCCTAAGGACTTGGACACTTGCAATAAAGAA  1500
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RESULT 5
AX403530
LOCUS       AX403530               1728 bp    DNA     linear   PAT 14-JUN-2002
DEFINITION  Sequence 417 from Patent WO0073454.
ACCESSION   AX403530
VERSION     AX403530.1  GI:21437007
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Ashkenazi,A.J., Baker,K.P., Botstein,D., Desnoyers,L., Eaton,D.,
            Ferrara,N., Gerber,H., Gerritsen,M., Goddard,A., Godowski,P.,
            Grimaldi,C.J., Gurney,A.L., Kljavin,I., Napier,M.A., Pan,J.,
            Paoni,N.F., Roy,M., Stewart,T.A., Tumas,D., Watanabe,C.K.,
            Williams,P., Wood,W.I. and Zhang,Z.
  TITLE     Secreted and transmembrane polypeptides and nucleic acids encoding
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  JOURNAL   Patent: WO 0073454-A 417 07-DEC-2000;
            Genentech Inc. (US)
FEATURES             Location/Qualifiers
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ORIGIN

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  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1728;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CAGCCGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCC 60
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RESULT 6
AY359069
LOCUS       AY359069                1728 bp    mRNA    linear   PRI 03-OCT-2003
DEFINITION  Homo sapiens clone DNA67004 C11orf15 (UNQ712) mRNA, complete cds.
ACCESSION   AY359069
VERSION     AY359069.1  GI:37183255
KEYWORDS    FLI_CDNA.
SOURCE      Homo sapiens (human)
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            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1728)
  AUTHORS   Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,
            Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B.,
            Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E.,
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            Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S.,
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            Schoenfeld,J., Seshagiri,S., Simmons,L., Singh,J., Smith,V.,
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            Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z.,
            Goddard,A., Wood,W.I. and Godowski,P.
  TITLE     The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
            Effort to Identify Novel Human Secreted and Transmembrane Proteins:
            A Bioinformatics Assessment
  JOURNAL   Genome Res. 13 (10), 2265-2270 (2003)
   PUBMED   12975309
REFERENCE   2  (bases 1 to 1728)
  AUTHORS   Clark,H.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
            Inc., 1 DNA Way, South San Francisco, CA 94080, USA
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ORIGIN

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  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1728;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CAGCCGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CAGCCGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCC 60

Qy         61 GGTCGCGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCCAGCGATGGCGACCCTGTGGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGTCGCGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCCAGCGATGGCGACCCTGTGGGG 120

Qy        121 AGGCCTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTTCCGTGCTGCT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AGGCCTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTTCCGTGCTGCT 180

Qy        181 GCTGGCGCAGCTGTCAGACGCCGCCAAGAATTTCGAGGATGTCAGATGTAAATGTATCTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCTGGCGCAGCTGTCAGACGCCGCCAAGAATTTCGAGGATGTCAGATGTAAATGTATCTG 240

Qy        241 CCCTCCCTATAAAGAAAATTCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CCCTCCCTATAAAGAAAATTCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTG 300

Qy        301 TGATTGCCTTCATGTTGTGGAGCCCATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGATTGCCTTCATGTTGTGGAGCCCATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTG 360

Qy        361 TCTACGCTGTGAATGCAAATATGAAGAAAGAAGCTCTGTCACAATCAAGGTTACCATTAT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TCTACGCTGTGAATGCAAATATGAAGAAAGAAGCTCTGTCACAATCAAGGTTACCATTAT 420

Qy        421 AATTTATCTCTCCATTTTGGGCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AATTTATCTCTCCATTTTGGGCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGA 480

Qy        481 GCCCATACTGAAGAGGCGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATAT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GCCCATACTGAAGAGGCGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATAT 540

Qy        541 TGGGGATCACCAGCCTTTTGCAAATGCACACGATGTGCTAGCCCGCTCCCGCAGTCGAGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TGGGGATCACCAGCCTTTTGCAAATGCACACGATGTGCTAGCCCGCTCCCGCAGTCGAGC 600

Qy        601 CAACGTGCTGAACAAGGTAGAATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAACGTGCTGAACAAGGTAGAATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCA 660

Qy        661 GCGAAAGTCTGTCTTTGACCGGCATGTTGTCCTCAGCTAATTGGGAATTGAATTCAAGGT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GCGAAAGTCTGTCTTTGACCGGCATGTTGTCCTCAGCTAATTGGGAATTGAATTCAAGGT 720

Qy        721 GACTAGAAAGAAACAGGCAGACAACTGGAAAGAACTGACTGGGTTTTGCTGGGTTTCATT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GACTAGAAAGAAACAGGCAGACAACTGGAAAGAACTGACTGGGTTTTGCTGGGTTTCATT 780

Qy        781 TTAATACCTTGTTGATTTCACCAACTGTTGCTGGAAGATTCAAAACTGGAAGCAAAAACT 840
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Db        781 TTAATACCTTGTTGATTTCACCAACTGTTGCTGGAAGATTCAAAACTGGAAGCAAAAACT 840

Qy        841 TGCTTGATTTTTTTTTCTTGTTAACGTAATAATAGAGACATTTTTAAAAGCACACAGCTC 900
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Qy        901 AAAGTCAGCCAATAAGTCTTTTCCTATTTGTGACTTTTACTAATAAAAATAAATCTGCCT 960
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Qy        961 GTAAATTATCTTGAAGTCCTTTACCTGGAACAAGCACTCTCTTTTTCACCACATAGTTTT 1020
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Qy       1021 AACTTGACTTTCAAGATAATTTTCAGGGTTTTTGTTGTTGTTGTTTTTTGTTTGTTTGTT 1080
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Qy       1081 TTGGTGGGAGAGGGGAGGGATGCCTGGGAAGTGGTTAACAACTTTTTTCAAGTCACTTTA 1140
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Db       1141 CTAAACAAACTTTTGTAAATAGACCTTACCTTCTATTTTCGAGTTTCATTTATATTTTGC 1200

Qy       1201 AGTGTAGCCAGCCTCATCAAAGAGCTGACTTACTCATTTGACTTTTGCACTGACTGTATT 1260
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Db       1201 AGTGTAGCCAGCCTCATCAAAGAGCTGACTTACTCATTTGACTTTTGCACTGACTGTATT 1260

Qy       1261 ATCTGGGTATCTGCTGTGTCTGCACTTCATGGTAAACGGGATCTAAAATGCCTGGTGGCT 1320
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Db       1261 ATCTGGGTATCTGCTGTGTCTGCACTTCATGGTAAACGGGATCTAAAATGCCTGGTGGCT 1320

Qy       1321 TTTCACAAAAAGCAGATTTTCTTCATGTACTGTGATGTCTGATGCAATGCATCCTAGAAC 1380
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Qy       1441 ACTCATCTTCTAGTACCTTTAAGGACAAATCCTAAGGACTTGGACACTTGCAATAAAGAA 1500
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Qy       1501 ATTTTATTTTAAACCCAAGCCTCCCTGGATTGATAATATATACACATTTGTCAGCATTTC 1560
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Db      1561 CGGTCGTGGTGAGAGGCAGCTGTTTGAGCTCCAATATGTGCAGCTTTGAACTAGGGCTGG 1620

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Db      1621 GGTTGTGGGTGCCTCTTCTGAAAGGTCTAACCATTATTGGATAACTGGCTTTTTTCTTCC 1680

Qy      1681 TATGTCCTCTTTGGAATGTAACAATAAAAATAATTTTTGAAACATCAA 1728

Db      1681 TATGTCCTCTTTGGAATGTAACAATAAAAATAATTTTTGAAACATCAA 1728


RESULT 7
BC040124
LOCUS       BC040124                1772 bp    mRNA    linear   PRI 07-OCT-2003
DEFINITION  Homo sapiens chromosome 11 open reading frame 15, mRNA (cDNA clone
            MGC:48749 IMAGE:6053804), complete cds.
ACCESSION   BC040124
VERSION     BC040124.1  GI:25304014
KEYWORDS    MGC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1772)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
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            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
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            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
  MEDLINE   22388257
   PUBMED   12477932
REFERENCE   2  (bases 1 to 1772)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-NOV-2002) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Institute for Systems Biology
            http://www.systemsbiology.org
            contact: amadan@systemsbiology.org
            Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha
            Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 84 Row: o Column: 11
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 11034854.
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                     /note="Vector: pCMV-SPORT6"
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                     /db_xref="LocusID:56674"
                     /translation="MATLWGGLLRLGSLLSLSCLALSVLLLAQLSDAAKNFEDVRCKC
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                     VTIIIYLSILGLLLLYMVYLTLVEPILKRRLFGHAQLIQSDDDIGDHQPFANAHDVLA
                     RSRSRANVLNKVEYAQQRWKLQVQEQRKSVFDRHVVLS"
ORIGIN

  Query Match             97.8%;  Score 1690.4;  DB 9;  Length 1772;
  Best Local Similarity   99.5%;  Pred. No. 0;
  Matches 1719;  Conservative    0;  Mismatches    1;  Indels    8;  Gaps    2;

Qy          1 CAGCCGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCC 60

Db         40 CAGCCGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCC 99

Qy         61 GGTCGCGGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCCAGCGATGGCGACCCTGTGGGG 120

Db        100 GGTCGCGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCCAGCGATGGCGACCCTGTGGGG 159

Qy        121 AGGCCTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTTCCGTGCTGCT 180

Db        160 AGGCCTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTTCCGTGCTGCT 219

Qy        181 GCTGGCGCAGCTGTCAGACGCCGCCAAGAATTTCGAGGATGTCAGATGTAAATGTATCTG 240

Db        220 GCTGGCGCAGCTGTCAGACGCCGCCAAGAATTTCGAGGATGTCAGATGTAAATGTATCTG 279

Qy        241 CCCTCCCTATAAAGAAAATTCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTG 300

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Qy        301 TGATTGCCTTCATGTTGTGGAGCCCATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTG 360

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Db        640 CAACGTGCTGAACAAGGTAGAATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCA 699

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Db        700 GCGAAAGTCTGTCTTTGACCGGCATGTTGTCCTCAGCTAATTGGGAATTGAATTCAAGGT 759
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Qy        781 TTAATACCTTGTTGATTTCACCAACTGTTGCTGGAAGATTCAAAACTGGAAGCAAAAACT 840
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Qy       1081 TTGGTGGGAGAGGGGAGGGATGCCTGGGAAGTGGTTAACAACTTTTTTCAAGTCACTTTA 1140
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Qy       1261 ATCTGGGTATCTGCTGTGTCTGCACTTCATGGTAAACGGGATCTAAAATGCCTGGTGGCT 1320
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Qy       1321 TTTCACAAAAAGCAGATTTTCTTCATGTACTGTGATGTCTGATGCAATGCATCCTAGAAC 1380
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Qy       1621 GGTTGTGGGTGCCTCTTCTGAAAGGTCTAACCATTATTGGATAACTGGCTTTTTTCTTCC 1680
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RESULT 8
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BD222662
LOCUS       BD222662                1834 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Human signal peptide-containing protein.
ACCESSION   BD222662
VERSION     BD222662.1  GI:33032432
KEYWORDS    JP 2002519030-A/8.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1834)
  AUTHORS   Lal,P., Tang,Y.T., Gorgone,G.A., Corley,N.C., Guegler,K.J.,
            Baughn,M.R., Akerblom,I.E., Young,J.A., Yue,H., Patterson,C.,
            Reddy,R., Hillman,J.L. and Bandman,O.
  TITLE     Human signal peptide-containing protein
  JOURNAL   Patent: JP 2002519030-A 8 02-JUL-2002;
            INCYTE PHARMACEUTICALS INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002519030-A/8
            PD   02-JUL-2002
            PF   25-JUN-1999 JP 2000557363
            PR   26-JUN-1998 US    60/090762,31-JUL-1998 US    60/094983 PR
            01-OCT-1998 US    60/102686,11-DEC-1998 US    60/112129 PI   PREETI
            LAL,Y TOM TANG,GINA A GORGONE,NEIL C CORLEY,KARL J  PI   GUEGLER,
            PI   MARIAH R BAUGHN,INGRID E AKERBLOM,JANICE AU YOUNG,HENRY YUE,
            PI   CHANDRA PATTERSON,ROOPA REDDY,JENNIFER L HILLMAN,OLGA BANDMAN
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ORIGIN

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Qy        250 TAAAGAAAATTCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTGTGATTGCCT 309
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Qy        310 TCATGTTGTGGAGCCCATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTGTCTACGCTG 369
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Db        401 TGAATGCAAATATGAAGAAAGAAGCTCTGTCACAATCAAGGTTACCATTATAATTTATCT 460

Qy        430 CTCCATTTTGGGCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGAGCCCATACT 489
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        461 CTCCATTTTGGGCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGAGCCCATACT 520

Qy        490 GAAGAGGCGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATATTGGGGATCA 549
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        521 GAAGAGGCGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATATTGGGGATCA 580

Qy        550 CCAGCCTTTTGCAAATGCACACGATGTGCTAGCCCGCTCCCGCAGTCGAGCCAACGTGCT 609
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        581 CCAGCCTTTTGCAAATGCACACGATGTGCTAGCCCGCTCCCGCAGTCGAGCCAACGTGCT 640

Qy        610 GAACAAGGTAGAATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCAGCGAAAGTC 669
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Db        641 GAACAAGGTAGAATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCAGCGAAAGTC 700

Qy        670 TGTCTTTGACCGGCATGTTGTCCTCAGCTAATTGGGAATTGAATTCAAGGTGACTAGAAA 729
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Db        701 TGTCTTTGACCGGCATGTTGTCCTCAGCTAATTGGGAATTGAATTCAAGGTGACTAGAAA 760

Qy        730 GAAACAGGCAGACAACTGGAAAGAACTGACTGGGTTTTGCTGGGTTTCATTTTAATACCT 789
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        761 GAAACAGGCAGACAACTGGAAAGAACTGACTGGGTTTTGCTGGGTTTCATTTTAATACCT 820

Qy        790 TGTTGATTTCACCAACTGTTGCTGGAAGATTCAAAACTGGAAGCAAAAACTTGCTTGATT 849
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Qy        850 TTTTTTTCTTGTTAACGTAATAATAGAGACATTTTTAAAAGCACACAGCTCAAAGTCAGC 909
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Qy        910 CAATAAGTCTTTTCCTATTTGTGACTTTTACTAATAAAAATAAATCTGCCTGTAAATTAT 969
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Db        941 CAATAAGTCTTTTCCTATTTGTGACTTTTACTAATAAAAATAAATCTGCCTGTAAATTAT 1000

Qy        970 CTTGAAGTCCTTTACCTGGAACAAGCACTCTCTTTTTCACCACATAGTTTTAACTTGACT 1029
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1001 CTTGAAGTCCTTTACCTGGAACAAGCACTCTCTTTTTCACCACATAGTTTTAACTTGACT 1060

Qy       1030 TTCAAGATAATTTTCAGGGTTTTTGTTGTTGTTGTTTTTTGTTTGTTTGTTTTGGTGGGA 1089
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1061 TTCAAGATAATTTTCAGGGTTTTTGTTGTTGTTGTTTTTTGTTTGTTTGTTTTGGTGGGA 1120

Qy       1090 GAGGGGAGGGATGCCTGGGAAGTGGTTAACAACTTTTTTCAAGTCACTTTACTAAACAAA 1149
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1121 GAGGGGAGGGATGCCTGGGAAGTGGTTAACAACTTTTTTCAAGTCACTTTACTAAACAAA 1180

Qy       1150 CTTTTGTAAATAGACCTTACCTTCTATTTTCGAGTTTCATTTATATTTTGCAGTGTAGCC 1209
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Db       1181 CTTTTGTAAATAGACCTTACCTTCTATTTTCGAGTTTCATTTATATTTTGCAGTGTAGCC 1240

Qy       1210 AGCCTCATCAAAGAGCTGACTTACTCATTTGACTTTTGCACTGACTGTATTATCTGGGTA 1269
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Db       1241 AGCCTCATCAAAGAGCTGACTTACTCATTTGACTTTTGCACTGACTGTGTTATCTGGGTA 1300

Qy       1270 TCTGCTGTGTCTGCACTTCATGGTAAACGGGATCTAAAATGCCTGGTGGCTTTTCACAAA 1329
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1301 TCTGCTGTGTCTGCACTTCATGGTAAACGGGATCTAAAATGCCTGGTGGCTTTTCACAAA 1360

Qy       1330 AAGCAGATTTTCTTCATGTACTGTGATGTCTGATGCAATGCATCCTAGAACAAACTGGCC 1389
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1361 AAGCAGATTTTCTTCATGTACTGTGATGTCTGATGCAATGCATCCTAGAACAAACTGGCC 1420

Qy       1390 ATTTGCTAGTTTACTCTAAAGACTAAACATAGTCTTGGTGTGTGTGGTCTTACTCATCTT 1449
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1421 ATTTGCTAGTTTACTCTAAAGACTAAACATAGTCTTGGTGTGTGTGGTCTTACTCATCTT 1480

Qy       1450 CTAGTACCTTTAAGGACAAATCCTAAGGACTTGGACACTTGCAATAAAGAAATTTTATTT 1509
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db       1481 CTAGTACCTTTAAGGACAAATCCTAAGGACTTGGACACTTGCAATAAAGAAATTTTATTT 1540

Qy       1510 TAAACCCAAGCCTCCCTGGATTGATAATATATACACATTTGTCAGCATTTCCGGTCGTGG 1569
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Db       1541 TAAACCCAAGCCTCCCTGGATTGATAATATATACACATTTGTCAGCATTTCCGGTCGTGG 1600

Qy       1570 TGAGAGGCAGCTGTTTGAGCTCCAATATGTGCAGCTTTGAACTAGGGCTGGGGTTGTGGG 1629
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Db       1601 TGAGAGGCAGCTGTTTGAGCTCCAATGTGTGCAGCTTTGAACTAGGGCTGGGGTTGTGGG 1660

Qy       1630 TGCCTCTTCTGAAAGGTCTAACCATTATTGGATAACTGGCTTTTTTCTTCCTATGTCCTC 1689
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Db       1661 TGCCTCTTCTGAAAGGTCTAACCATTATTGGATAACTGGCTTTTTTCT-------TCCTC 1713

Qy       1690 TTTGGAATGTAACAATAAAAATAATTTTTGAAACATCAA 1728
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Db       1714 TTTGGAATGTAACAATAAAAATAATTTTTGAAACATCCA 1752
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RESULT 9
BD127721

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LOCUS       BD127721                1694 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Primer for synthesizing full-length cDNA and use thereof.
ACCESSION   BD127721
VERSION     BD127721.1  GI:23222666
KEYWORDS    JP 2002017375-A/3152.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1694)
  AUTHORS   Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y.,
            Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
            Koga,H.
  TITLE     Primer for synthesizing full-length cDNA and use thereof
  JOURNAL   Patent: JP 2002017375-A 3152 22-JAN-2002;
            HELIX RESEARCH INSTITUTE
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002017375-A/3152
            PD   22-JAN-2002
            PF   07-JUL-2000 JP 2000253172
            PI   TOSHIO OTA,TETSUO NISHIKAWA,TAKAO ISOGAI,KOJI HAYASHI,SHIZUKO
            PI   ISHII,
            PI   YURI KAWAI,AI WAKAMATSU,TOMOYASU SUGIYAMA,KEIICHI NAGAI, PI
            SHINICHI KOJIMA,
            PI   TETSUJI OTSUKI,HISASHI KOGA
            PC
            C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC
             10,
            PC   C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00 CC
             Primer for synthesizing full-length cDNA and use thereof FH   Key
                     Location/Qualifiers
            FT   CDS             (79). .(672).
FEATURES             Location/Qualifiers
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ORIGIN
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  Matches 1691;  Conservative    0;  Mismatches    3;  Indels    7;  Gaps    1;

Qy         26 AGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCCGGTCGCGGGGGCTCCGGGCTGTGGG 85
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Db          1 AGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCCGGTCGCGGGGGCTCCGGGCTGTGGG 60

Qy         86 ACCGCTGGGCCCCCAGCGATGGCGACCCTGTGGGGAGGCCTTCTTCGGCTTGGCTCCTTG 145
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACCGCTGGGCCCCCAGCGATGGCGACCCTGTGGGGAGGCCTTCTTCGGCTTGGCTCCTTG 120

Qy        146 CTCAGCCTGTCGTGCCTGGCGCTTTCCGTGCTGCTGCTGGCGCAGCTGTCAGACGCCGCC 205
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Db        121 CTCAGCCTGTCGTGCCTGGCGCTTTCCGTGCTGCTGCTGGCGCAGCTGTCAGACGCCGCC 180
Qy        206 AAGAATTTCGAGGATGTCAGATGTAAATGTATCTGCCCTCCCTATAAAGAAAATTCTGGG 265
Db        181 AAGAATTTCGAGGATGTCAGATGTAAATGTATCTGCCCTCCCTATAAAGAAAATTCTGGG 240
Qy        266 CATATTTATAATAAGAACATATCTCAGAAAGATTGTGATTGCCTTCATGTTGTGGAGCCC 325
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Qy        326 ATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTGTCTACGCTGTGAATGCAAATATGAA 385
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Qy        386 GAAAGAAGCTCTGTCACAATCAAGGTTACCATTATAATTTATCTCTCCATTTTGGGCCTT 445
Db        361 GAAAGAAGCTCTGTCACAATCAAGGTTACCATTATAATTTATCTCTCCATTTTGGGCCTT 420
Qy        446 CTACTTCTGTACATGGTATATCTTACTCTGGTTGAGCCCATACTGAAGAGGCGCCTCTTT 505
Db        421 CTACTTCTGTACATGGTATATCTTACTCTGGTTGAGCCCATACTGAAGAGGCGCCTCTTT 480
Qy        506 GGACATGCACAGTTGATACAGAGTGATGATGATATTGGGGATCACCAGCCTTTTGCAAAT 565
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Qy        566 GCACACGATGTGCTAGCCCGCTCCCGCAGTCGAGCCAACGTGCTGAACAAGGTAGAATAT 625
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Qy        626 GCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCAGCGAAAGTCTGTCTTTGACCGGCAT 685
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Qy        686 GTTGTCCTCAGCTAATTGGGAATTGAATTCAAGGTGACTAGAAAGAAACAGGCAGACAAC 745
Db        661 GTTGTCCTCAGCTAATTGGGAATTGAATTCAAGGTGACTAGAAAGAAACAGGCAGACAAC 720
Qy        746 TGGAAAGAACTGACTGGGTTTTGCTGGGTTTCATTTTAATACCTTGTTGATTTCACCAAC 805
Db        721 TGGAAAGAACTGACTGGGTTTTGCTGGGTTTCATTTTAATACCTTGTTGATTTCACCAAC 780
Qy        806 TGTTGCTGGAAGATTCAAAACTGGAAGCAAAAACTTGCTTGATTTTTTTTTCTTGTTAAC 865
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Qy        866 GTAATAATAGAGACATTTTTAAAAGCACACAGCTCAAAGTCAGCCAATAAGTCTTTTCCT 925
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Qy        986 TGGAACAAGCACTCTCTTTTTCACCACATAGTTTTAACTTGACTTTCAAGATAATTTTCA 1045
Db        961 TGGAACAAGCACTCTCTTTTTCACCACATAGTTTTAACTTGACTTTCAAGATAATTTTCA 1020
Qy       1046 GGGTTTTTGTTGTTGTTGTTTTTTGTTTGTTTGTTTTGGTGGGAGAGGGGAGGGATGCCT 1105
Db       1021 GGGTTTTTGTTGTTGTTGTTTTTTGTTTGTTTGTTTTGGTGGGAGAGGGGAGGGATGCCT 1080
Qy       1106 GGGAAGTGGTTAACAACTTTTTTCAAGTCACTTTACTAAACAAACTTTTGTAAATAGACC 1165
Db       1081 GGGAAGTGGTTAACAACTTTTTTCAAGTCACTTTACTAAACAAACTTTTGTAAATAGACC 1140
Qy       1166 TTACCTTCTATTTTCGAGTTTCATTTATATTTTGCAGTGTAGCCAGCCTCATCAAAGAGC 1225
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Qy       1226 TGACTTACTCATTTGACTTTTGCACTGACTGTATTATCTGGGTATCTGCTGTGTCTGCAC 1285
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Qy       1286 TTCATGGTAAACGGGATCTAAAATGCCTGGTGGCTTTTCACAAAAAGCAGATTTTCTTCA 1345
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Qy       1526 TGGATTGATAATATATACACATTTGTCAGCATTTCCGGTCGTGGTGAGAGGCAGCTGTTT 1585
Db       1501 TGGATTGATAATATATACACATTTGTCAGCATTTCCGGTCGTGGTGAGAGGCAGCTGTTT 1560
Qy       1586 GAGCTCCAATATGTGCAGCTTTGAACTAGGGCTGGGGTTGTGGGTGCCTCTTCTGAAAGG 1645
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Qy       1646 TCTAACCATTATTGGATAACTGGCTTTTTTCTTCCTATGTCCTCTTTGGAATGTAACAAT 1705
Db       1621 TCTAACCATTATTGGATAACTGGCTTTTTTCT-------TCCCCTTTGGAATGTAACAAT 1673
Qy       1706 AAAAATAATTTTTGAAACATC 1726
Db       1674 AAAAATAATTTTCGAAACATC 1694
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RESULT 10
AK074677

LOCUS	AK074677 1694 bp mRNA linear PRI 03-SEP-2002
DEFINITION	Homo sapiens cDNA FLJ90196 fis, clone MAMMA1001344.
ACCESSION	AK074677
VERSION	AK074677.1 GI:22760273
KEYWORDS	oligo capping; fis (full insert sequence).
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1
AUTHORS	Isogai,T., Ota,T., Nishikawa,T., Hayashi,K., Otsuki,T., Sugiyama,T., Suzuki,Y., Nagai,K., Sugano,S., Ishii,S., Kawai-Hio,Y., Saito,K., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Kojima,S., Nagahari,K., Masuho,Y., Ono,T., Okano,K., Yoshikawa,Y., Aotsuka,S., Sasaki,N., Hattori,A., Okumura,K., Iwayanagi,T. and Ninomiya,K.
TITLE	NEDO human cDNA sequencing project
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 1694)
AUTHORS	Isogai,T. and Otsuki,T.
TITLE	Direct Submission
JOURNAL	Submitted (25-MAR-2002) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
COMMENT	NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; cDNA 5'- & 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.).
FEATURES	Location/Qualifiers
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ORIGIN

  Query Match             96.8%;  Score 1672.2;  DB 9;  Length 1694;
  Best Local Similarity   99.4%;  Pred. No. 0;
  Matches 1691;  Conservative    0;  Mismatches    3;  Indels    7;  Gaps    1;

Qy         26 AGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCCGGTCGCGGGGGCTCCGGGCTGTGGG 85
Db          1 AGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCCGGTCGCGGGGGCTCCGGGCTGTGGG 60

Qy         86 ACCGCTGGGCCCCCAGCGATGGCGACCCTGTGGGGAGGCCTTCTTCGGCTTGGCTCCTTG 145
Db         61 ACCGCTGGGCCCCCAGCGATGGCGACCCTGTGGGGAGGCCTTCTTCGGCTTGGCTCCTTG 120

Qy        146 CTCAGCCTGTCGTGCCTGGCGCTTTCCGTGCTGCTGCTGGCGCAGCTGTCAGACGCCGCC 205
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Qy        206 AAGAATTTCGAGGATGTCAGATGTAAATGTATCTGCCCTCCCTATAAAGAAAATTCTGGG 265
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Qy        326 ATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTGTCTACGCTGTGAATGCAAATATGAA 385
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Qy        386 GAAAGAAGCTCTGTCACAATCAAGGTTACCATTATAATTTATCTCTCCATTTTGGGCCTT 445
Db        361 GAAAGAAGCTCTGTCACAATCAAGGTTACCATTATAATTTATCTCTCCATTTTGGGCCTT 420

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Qy        506 GGACATGCACAGTTGATACAGAGTGATGATGATGATATTGGGGATCACCAGCCTTTTGCAAAT 565
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Qy        566 GCACACGATGTGCTAGCCCGCTCCCGCAGTCGAGCCAACGTGCTGAACAAGGTAGAATAT 625
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Qy        626 GCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCAGCGAAAGTCTGTCTTTGACCGGCAT 685
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Qy        686 GTTGTCCTCAGCTAATTGGGAATTGAATTCAAGGTGACTAGAAAGAAACAGGCAGACAAC 745
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Qy        746 TGGAAAGAACTGACTGGGTTTTGCTGGGTTTCATTTTAATACCTTGTTGATTTCACCAAC 805
Db        721 TGGAAAGAACTGACTGGGTTTTGCTGGGTTTCATTTTAATACCTTGTTGATTTCACCAAC 780

Qy        806 TGTTGCTGGAAGATTCAAAACTGGAAGCAAAAACTTGCTTGATTTTTTTTTCTTGTTAAC 865
Db        781 TGTTGCTGGAAGATTCAAAACTGGAAGCAAAAACTTGCTTGATTTTTTTTTCTTGTTAAC 840

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Qy        926 ATTTGTGACTTTTACTAATAAAAATAAATCTGCCTGTAAATTATCTTGAAGTCCTTTACC 985
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Qy        986 TGGAACAAGCACTCTCTTTTTCACCACATAGTTTTAACTTGACTTTCAAGATAATTTTCA 1045
Db        961 TGGAACAAGCACTCTCTTTTTCACCACATAGTTTTAACTTGACTTTCAAGATAATTTTCA 1020

Qy       1046 GGGTTTTTGTTGTTGTTGTTTTTTGTTTGTTTGTTTTGGTGGGAGAGGGGAGGGATGCCT 1105
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Qy       1106 GGGAAGTGGTTAACAACTTTTTTCAAGTCACTTTACTAAACAAACTTTTGTAAATAGACC 1165
Db       1081 GGGAAGTGGTTAACAACTTTTTTCAAGTCACTTTACTAAACAAACTTTTGTAAATAGACC 1140

Qy       1166 TTACCTTCTATTTTCGAGTTTCATTTATATTTTGCAGTGTAGCCAGCCTCATCAAAGAGC 1225
Db       1141 TTACCTTCTATTTTCGAGTTTCATTTATATTTTGCAGTGTAGCCAGCCTCATCAAAGAGC 1200

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Qy       1406 TAAAGACTAAACATAGTCTTGGTGTGTGTGGTCTTACTCATCTTCTAGTACCTTTAAGGA 1465
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Db       1501 TGGATTGATAATATATACACATTTGTCAGCATTTCCGGTCGTGGTGAGAGGCAGCTGTTT 1560

Qy       1586 GAGCTCCAATATGTGCAGCTTTGAACTAGGGCTGGGGTTGTGGGTGCCTCTTCTGAAAGG 1645
Db       1561 GAGCTCCAATGTGTGCAGCTTTGAACTAGGGCTGGGGTTGTGGGTGCCTCTTCTGAAAGG 1620

Qy       1646 TCTAACCATTATTGGATAACTGGCTTTTTTCTTCCTATGTCCTCTTTGGAATGTAACAAT 1705
Db       1621 TCTAACCATTATTGGATAACTGGCTTTTTTCT-------TCCCCTTTGGAATGTAACAAT 1673

Qy       1706 AAAAATAATTTTTGAAACATC 1726
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RESULT 11
AR352701
LOCUS       AR352701               1734 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 108 from patent US 6590075.
ACCESSION   AR352701
VERSION     AR352701.1  GI:33757959
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
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REFERENCE   1  (bases 1 to 1734)
  AUTHORS   Ruben,S.M., Rosen,C.A., Fischer,C.L., Soppet,D.R., Carter,K.C.,
            Bednarik,D.P., Endress,G.A., Yu,G.-L., Ni,J., Feng,P., Young,P.E.,
            Greene,J.M., Ferrie,A.M., Duan,R., Hu,J.-S., Florence,K.A.,
            Olsen,H.S., Ebner,R., Brewer,L.A. and Shi,Y.
  TITLE     Secreted protein HODAZ50
  JOURNAL   Patent: US 6590075-A 108 08-JUL-2003;
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             95.4%;  Score 1649.2;  DB 6;  Length 1734;
  Best Local Similarity   99.1%;  Pred. No. 0;
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Db          1 CGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCCGGTC 60

Qy         65 GCGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCCAGCGATGGCGACCCTGTGGGGAGGC 124
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Db         61 GCGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCCAGCGATGGCGACCCTGTGGGGAGGC 120

Qy        125 CTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTTCCGTGCTGCTGCTG 184
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Db        121 CTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTTCCGTGCTGCTGCTG 180

Qy        185 GCGCAGCTGTCAGACGCCGCCAAGAATTTCGAGGATGTCAGATGTAAATGTATCTGCCCT 244
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Db        181 GCGCATGT-NCAGACGCCGCCAAGAATTTCGAGGATGTCAGATGTAAATGTATCTGCCCT 239

Qy        245 CCCTATAAAGAAAATTCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTGTGAT 304
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Db        240 CCCTATAAAGAAAATTCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTGTGAT 299

Qy        305 TGCCTTCATGTTGTGGAGCCCATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTGTCTA 364
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Qy        365 CGCTGTGAATGCAAATATGAAGAAAGAAGCTCTGTCACAATCAAGGTTACCATTATAATT 424
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Qy        425 TATCTCTCCATTTTGGGCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGAGCCC 484
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Qy        605 GTGCTGAACAAGGTAGAATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCAGCGA 664
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Db        600 GTGCTGAACAAGGTAGAATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCAGCGA 659

Qy        665 AAGTCTGTCTTTGACCGGCATGTTGTCCTCAGCTAATT-GGGAATTGAATTCAAGGTGAC 723
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Qy        724 TAGAAAGAAACAGGCAGACAACT-GGAAAGAACTGACTGGG-TTTTGCTGGGTTTCATTT 781
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Qy        782 TAATACCTTGTTGATTTCACCAACTGTTGCTGGAAGATTCAAAACTGGAAGCAAAAACTT 841
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Db        780 TAATACCTTGTTGATTTCACCAACTGTTGCTGGAAGATTCAAAACTGGAAGCAAAAACTT 839

Qy        842 GCTTGATTTTTTTTTCTTGTTAACGTAATAATAGAGACATTTTTAAAAGCACACAGCTCA 901
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Qy        902 AAGTCAGCCAATAAGTCTTTTCCTATTTGTGACTTTTACTAATAAAAATAAATCTGCCTG 961
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Qy        962 TAAATTATCTTGAAGTCCTTTACCTGGAACAAGCACTCTCTTTTTCACCACATAGTTTTA 1021
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Qy       1022 ACTTGACTTTCAAGATAATTTTCAGGGTTTTTGTTGTTGTTGTTTTTTGTTTGTTTGTTT 1081
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RESULT 12
BD195646
LOCUS       BD195646               1734 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  70 human secreted proteins.
ACCESSION   BD195646
VERSION     BD195646.1  GI:33005416
KEYWORDS    JP 2002519990-A/107.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 1734)
  AUTHORS   Ruben,S.M., Rosen,C.A., Fischer,C.L., Soppet,D.R., Carter,K.C.,
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            Bednarik,D.P., Endress,G.A., Yu,G.L., N,J., Feng,P., Young,P.E.,
            Greene,J.M., Ferrie,A.M., Duan,R., Hu,J.S., Florence,K.A.,
            Olsen,H.S., Ebner,R., Brewer,L.A., Moore,P.A., Shi,Y.,
            Lafleur,D.W., Li,Y., Zeng,Z. and Kyaw,H.
  TITLE     70 human secreted proteins
  JOURNAL   Patent: JP 2002519990-A 107 02-JUL-2002;
            HUMAN GENOME SCIENCES INC
COMMENT     OS   Unidentified
            PN   JP 2002519990-A/107
            PD   02-JUL-2002
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            PI   KENNETH C CARTER,DANIEL P BEDNARIK,GREGORY
            A ENDRESS,GUO LIANG
            PI   YU,JIAN NI,
            PI   PING FENG,PAUL E YOUNG,JOHN M GREENE,ANN
            M FERRIE,ROXANNE DUAN,
            PI   JING SHAN HU,KIMBERLY A FLORENCE,HENRIK
            S OLSEN,REINHARD EBNER,
            PI   LAURIE A BREWER,PAUL A MOORE,YANGGU SHI,DAVID W LAFLEUR PI
            ,YI LI,ZHIZHEN ZENG,
            PI   HLA KYAW
            PC   C12N15/12,C12N5/10,C12N1/21,C07K14/47,C07K16/18,C12Q1/68, PC
            G01N33/50,
            PC   G01N33/53,G01N33/68,A61K38/17
            CC   Strandedness: Double;
            CC   Topology: Linear;
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            FH   Key             Location/Qualifiers
            FT   source          1. .1734
            FT                   /organism='Unidentified'.
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ORIGIN

  Query Match             95.4%;  Score 1649.2;  DB 6;  Length 1734;
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Qy          5 CGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCCGGTC 64
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Qy        902 AAGTCAGCCAATAAGTCTTTTCCTATTTGTGACTTTTACTAATAAAAATAAATCTGCCTG 961
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Qy       1322 TTCACAAAAAGCAGATTTTCTTCATGTACTGTGATGTCTGATGCAATGCATCCTAGAACA 1381
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Db       1320 TTCACAAAAAGCAGATTTTCTTCATGTACTGTGATGTCTGATGCAATGCATCCTAGAACA 1379

Qy       1382 AACTGGCCATTTGCTAGTTTACTCTAAAGACTAAACATAGTCTTGGTGTGTGTGGTCTTA 1441
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Qy       1442 CTCATCTTCTAGTACCTTTAAGGACAAATCCTAAGGACTTGGACACTTGCAATAAAGAAA 1501
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Db       1440 CTCATCTTCTAGTACCTTTAAGGACAAATCCTAAGGACTTGGACACTTGCAATAAAGAAA 1499

Qy       1502 TTTTATTTTAAACCCAAGCCTCCCTGGATTGATAATATATACACATTTGTCAGCATTTCC 1561
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Qy       1562 GGTCGTGGTGAGAGGCAGCTGTTTGAGCTCCAATATGTGCAGCTTTGAACTAGGGCTGGG 1621
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Qy       1622 GTTGTGGGTGCCTCTTCTGAAAGGTCTAACCATTATTGGATAACTGGCTTTTTTCTTCCT 1681
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Qy       1682 ATGTCCTCTTTGGAATGTAACAATAAAAATAATTTTTGAAACATCAA 1728
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RESULT 13
AR352639
LOCUS       AR352639               1772 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 46 from patent US 6590075.
ACCESSION   AR352639
VERSION     AR352639.1  GI:33757897
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1772)
  AUTHORS   Ruben,S.M., Rosen,C.A., Fischer,C.L., Soppet,D.R., Carter,K.C.,
            Bednarik,D.P., Endress,G.A., Yu,G.-L., Ni,J., Feng,P., Young,P.E.,
            Greene,J.M., Ferrie,A.M., Duan,R., Hu,J.-S., Florence,K.A.,
            Olsen,H.S., Ebner,R., Brewer,L.A. and Shi,Y.
  TITLE     Secreted protein HODAZ50
  JOURNAL   Patent: US 6590075-A 46 08-JUL-2003;
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             92.0%;  Score 1589.6;  DB 6;  Length 1772;
  Best Local Similarity   98.6%;  Pred. No. 0;
  Matches 1711;  Conservative    0;  Mismatches    9;  Indels   16;  Gaps   10;

Qy          1 CAGCCGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCC 60
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Db         27 CAGCCGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAG-CCGAGCCGGGAGCC 85

Qy         61 GGTCGCGGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCCAGCGATGGCGACCCTGTGGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         86 GGTCGCGGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCCAGCGATGGCGACCCTGTGGGG 145

Qy        121 AGGCCTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTTCCGTGCTGCT 180
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Db        146 AGGCCTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTTCCGTGCTGCT 205

Qy        181 GCTGGCGCAGCTGTCAGACGCCGCCAAGAATTTCGAGGATGTCAGATGTAAATGTATCTG 240
              ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        206 GCTGGCGCA-CTGTCAGACGCCGCCAAGAATTTCGAGGATGTCAGATGTAAATGTATCTG 264

Qy        241 CCCTCCCTATAAAG-AAAATTCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATT 299
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Db        265 CCCTCCCTATAAAGAAAAAATTCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATT 324

Qy        300 GTGATTGCCTTCATGTTGTGGAGCCCATGCCTGTGCGGGGGCCTGATGTAGAAGCATACT 359
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        325 GTGATTGCCTTCATGTTGTGGAGCCCATGCCTGTGCGGGGGCCTGATGTAGAAGCATACT 384

Qy        360 GTCTACGCTGTGAATGCAAATATGAAGAAAGAAGCTCTGTCACAATCAAGGTTACCATTA 419
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Qy        420 TAATTTATCTCTCCATTTTGGGCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTG 479
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Qy        480 AGCCCATACTGAAGAGGCGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATA 539
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Qy        540 TTGGGGATCACCAGCCTTTTGCAAATGCACACGATGTGCTAGCCCGCTCCCGCAGTCGAG 599
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Qy        600 CCAACGTGCTGAACAAGGTAGAATAT-GCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAG 658
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Db        625 CCAACGTGCTGAACAAGGTAGAATATGGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAG 684

Qy        659 CAGCG-AAAGTCTGTCTTTGACCGGCATGTTGTCCTCAGCTAATT-GGGAATTGAATTCA 716
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Db        685 CAGCGAAAAGTCTGTCTTTGACCGGCATGTTGTCCTCAGCTAATTGGGGAATTGAATTCA 744

Qy        717 AGGTGACTAGAAAGAAACAGGCAGACAACTGGAAA-GAACTGACTGGGTTTTGCTGGGTT 775
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Qy        776 TCATTTTAATACCTTGTTGATTTCACCAACTGTTGCTGGAAGATTCAAAACTGGAAGCAA 835
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Qy        896 AGCTCAAAGTCAGCCAATAAGTCTTTTCCTATTTGTGACTTTTACTAATAAAAATAAATC 955
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        925 AGCTCAAAGTCAGCCAATAAGTCTTTTCCTATTTGTGACTTTTACTAATAAAAATAAATC 984

Qy        956 TGCCTGTAAATTATCTT--GAAGTCCTTTACCTGGAACAAGCACTCTCTTTTTCACCACA 1013
              |||||||||| ||  ||    || |||||||||||||||||||||||||||||||||||||
Db        985 TGCCTGTAAAATAAATTAAAAAATCCTTTACCTGGAACAAGCACTCTCTTTTTCACCACA 1044

Qy       1014 TAGTTTTAACTTGACTTT-CAAGATAATTTTCAGGGTTTTTGTTGTTGTTGTTTTTTGTT 1072
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
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Qy       1193 TATTTTGCAGTGTAGCCAGCCTCATCAAAGAGCTGACTTACTCATTTGACTTTTGCACTG 1252
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Qy       1253 ACTGTATTATCTGGGTATCTGCTGTGTCTGCACTTCATGGTAAACGGGATCTAAAATGCC 1312
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Qy       1553 AGCATTTCCGGTCGTGGTGAGAGGCAGCTGTTTGAGCTCCAATATGTGCAGCTTTGAACT 1612
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RESULT 14
BD195584
LOCUS BD195584 1772 bp DNA linear PAT 17-JUL-2003
DEFINITION 70 human secreted proteins.
ACCESSION BD195584
VERSION BD195584.1 GI:33005354
KEYWORDS JP 2002519990-A/45.
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 1772)
AUTHORS Ruben,S.M., Rosen,C.A., Fischer,C.L., Soppet,D.R., Carter,K.C., Bednarik,D.P., Endress,G.A., Yu,G.L., N,J., Feng,P., Young,P.E., Greene,J.M., Ferrie,A.M., Duan,R., Hu,J.S., Florence,K.A., Olsen,H.S., Ebner,R., Brewer,L.A., Moore,P.A., Shi,Y.,
Lafleur,D.W., Li,Y., Zeng,Z. and Kyaw,H.
TITLE 70 human secreted proteins
JOURNAL Patent: JP 2002519990-A 45 02-JUL-2002;
HUMAN GENOME SCIENCES INC
COMMENT OS Unidentified
PN JP 2002519990-A/45
PD 02-JUL-2002
PF 06-MAR-1998 JP 1998538875
PR 07-MAR-1997 US 60/040162,07-MAR-1997 US 60/040333 PR
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PI STEVEN M RUBEN,CRAIG A ROSEN,CARRIE L FISCHER,DANIEL R SOPPET,
PI KENNETH C CARTER,DANIEL P BEDNARIK,GREGORY
A ENDRESS,GUO LIANG
PI YU,JIAN NI,
PI PING FENG,PAUL E YOUNG,JOHN M GREENE,ANN
M FERRIE,ROXANNE DUAN,
PI JING SHAN HU,KIMBERLY A FLORENCE,HENRIK
S OLSEN,REINHARD EBNER,
PI LAURIE A BREWER,PAUL A MOORE,YANGGU SHI,DAVID W LAFLEUR PI
,YI LI,ZHIZHEN ZENG,
PI HLA KYAW
PC C12N15/12,C12N5/10,C12N1/21,C07K14/47,C07K16/18,C12Q1/68, PC
G01N33/50,
PC G01N33/53,G01N33/68,A61K38/17
CC Strandedness: Double;
CC Topology: Linear;
CC 70 human secreted proteins
FH Key Location/Qualifiers

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FEATURES             Location/Qualifiers
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
ORIGIN

  Query Match             92.0%;  Score 1589.6;  DB 6;  Length 1772;
  Best Local Similarity   98.6%;  Pred. No. 0;
  Matches 1711;  Conservative    0;  Mismatches    9;  Indels   16;  Gaps   10;

Qy          1 CAGCCGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db         27 CAGCCGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAG-CCGAGCCGGGAGCC 85

Qy         61 GGTCGCGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCCAGCGATGGCGACCCTGTGGGG 120
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Qy        241 CCCTCCCTATAAAG-AAAATTCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATT 299
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Qy        540 TTGGGGATCACCAGCCTTTTGCAAATGCACACGATGTGCTAGCCCGCTCCCGCAGTCGAG 599
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Qy        600 CCAACGTGCTGAACAAGGTAGAATAT-GCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAG 658
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Db        625 CCAACGTGCTGAACAAGGTAGAATATGGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAG 684

Qy        659 CAGCG-AAAGTCTGTCTTTGACCGGCATGTTGTCCTCAGCTAATT-GGGAATTGAATTCA 716
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Db        685 CAGCGAAAAGTCTGTCTTTGACCGGCATGTTGTCCTCAGCTAATTGGGGAATTGAATTCA 744

Qy        717 AGGTGACTAGAAAGAAACAGGCAGACAACTGGAAA-GAACTGACTGGGTTTTGCTGGGTT 775
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Qy        896 AGCTCAAAGTCAGCCAATAAGTCTTTTCCTATTTGTGACTTTTACTAATAAAAATAAATC 955
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Db        985 TGCCTGTAAAATAAATTAAAAAATCCTTTACCTGGAACAAGCACTCTCTTTTTCACCACA 1044

Qy       1014 TAGTTTTAACTTGACTTT-CAAGATAATTTTCAGGGTTTTTGTTGTTGTTGTTTTTTGTT 1072
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DEFINITION  71 human secretory proteins.
ACCESSION   BD218614
VERSION     BD218614.1  GI:33028384
KEYWORDS    JP 2002520050-A/95.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1772)
  AUTHORS   Ruben,S.M., Komatsoulis,G., Duan,R.D., Rosen,C.A., Moore,P.A.,
            Shi,Y., Lafleur,D.W., Ebner,R., Olsen,H.S., Brewer,L.A.,
            Florence,K.A., Young,P.E., Mucenski,M., Endress,G.A. and
            Soppet,D.R.
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  TITLE     71 human secretory proteins
  JOURNAL   Patent: JP 2002520050-A 95 09-JUL-2002;
            HUMAN GENOME SCIENCES INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002520050-A/95
            PD   09-JUL-2002
            PF   14-JUL-1999 JP 2000560238
            PR   15-JUL-1998 US    60/092921,15-JUL-1998 US    60/092922 PR
            15-JUL-1998 US    60/092956
            PI   STEVEN M RUBEN,GEORGE KOMATSOULIS,ROXANNE
            D DUAN,CRAIG A ROSEN,
            PI   PAUL A MOORE,YANGGU SHI,DAVID W LAFLEUR,REINHARD EBNER,HENRIK
            PI   S OLSEN,
            PI   LAURIE A BREWER,KIMBERLY A FLORENCE,PAUL E YOUNG,MICHAEL  PI
            MUCENSKI,
            PI   GREGORY A ENDRESS,DANIEL R SOPPET
            PC   C12N15/09,C07H21/02,C07H21/04,C07K14/47,C07K16/18,C12N1/15, PC
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            PC   C12N1/21,C12N5/10,C12P21/02,G01N33/50,G01N33/68//C12Q1/68, PC
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            PC   C12N5/00
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  Matches 1711;  Conservative    0;  Mismatches    9;  Indels   16;  Gaps   10;

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Db         27 CAGCCGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAG-CCGAGCCGGGAGCC 85

Qy         61 GGTCGCGGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCCCAGCGATGGCGACCCTGTGGGG 120
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Qy        121 AGGCCTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTTCCGTGCTGCT 180
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Qy        241 CCCTCCCTATAAAG-AAAATTCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATT 299
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Db        565 TTGGGGATCACCAGCCTTTTGCAAATGCACACGATGTGCTAGCCCGCTCCCGCAGTCGAG 624

Qy        600 CCAACGTGCTGAACAAGGTAGAATAT-GCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAG 658
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Qy        659 CAGCG-AAAGTCTGTCTTTGACCGGCATGTTGTCCTCAGCTAATT-GGGAATTGAATTCA 716
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Qy        717 AGGTGACTAGAAAGAAACAGGCAGACAACTGGAAA-GAACTGACTGGGTTTTGCTGGGTT 775
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Qy        776 TCATTTTAATACCTTGTTGATTTCACCAACTGTTGCTGGAAGATTCAAAACTGGAAGCAA 835
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Qy        956 TGCCTGTAAATTATCTT--GAAGTCCTTTACCTGGAACAAGCACTCTCTTTTTCACCACA 1013
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Job time : 6725 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 20, 2004, 02:12:11 ; Search time 4580 Seconds
(without alignments)
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Perfect score: 1728
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c	5	913.8	52.9	1201	9	AL562476	AL562476 AL562476
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	9	893.8	51.7	1063	12	BM924942	BM924942 AGENCOURT
c	10	893.4	51.7	962	9	AL567498	AL567498 AL567498
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	42	747	43.2	747	12	BI756642	BI756642 603024028
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ALIGNMENTS

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DEFINITION AL542404 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE010YN08 5-PRIME, mRNA sequence.
ACCESSION AL542404
VERSION AL542404.2 GI:30547515
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1045)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 15, 2001 this sequence version replaced gi:12874416.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 6242.f For more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DE010DG04QP1&cluster=6242.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :

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           http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
           Faraday Avenue Genoscope sequence ID : CS0DE010DG04QP1.
FEATURES             Location/Qualifiers
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                     /clone_lib="Homo sapiens PLACENTA"
                     /note="Vector: pCMVSPORT_6; 1st strand cDNA was primed
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                     the Not I and EcoRV sites of the pCMVSPORT 6 vector.
                     Library was not normalized."
ORIGIN

  Query Match             54.8%;  Score 947.4;  DB 9;  Length 1045;
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Qy         80 TGTGGGACCGCTGGGCCCCCAGCGATGGCGACCCTGTGGGGAGGCCTTCTTCGGCTTGGC 139
              ||||||||||||||||:|||||||||||:|||||||||||||||||:||||||||:|||||
Db        110 TGTGGGACCGCTGGGCSCCCAGCGATGGSGACCCTGTGGGGAGGCSTTCTTCGGSTTGGC 169

Qy        140 TCCTTGCTCAGCCTGTCGTGCCTGGCGCTTTCCGTGCTGCTGCTGGCGCAGCTGTCAGAC 199
              |||||||||||||||||||||||||||:||||||||||:|||::||::||||:|||:|||:
Db        170 TCCTTGCTCAGCCTGTCGTGCCTGGSGCTTTCCGTGSTGSTGSKGGSGCAG-TGTSAGAS 228

Qy        200 GCCGCCAAGAATTTCGAGGATGTCAGATGTAAATGTATCTGCCCTCCCTATAAAGAAAAT 259
              |:||||||||||||:||||||||:|||||||||||||||||||||:|||||||||||||||
Db        229 GSCGCCAAGAATTTSGAGGATGTSAGATGTAAATGTATCTGCCCTCSCTATAAAGAAAAT 288

Qy        260 TCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTGTGATTGCCTTCATGTTGTG 319
              |||||||||||||||||||||||||||:|||||||||||||||||:||||||||||||||
Db        289 TCTGGGCATATTTATAATAAGAACATATCTSAGAAAGATTGTGATTGCSTTCATGTTGTG 348

Qy        320 GAGCCCATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTGTCTACGCTGTGAATGCAAA 379
              ||||:|||||||||||||||||||||||||||||||||||||||||||:||||||||||||
Db        349 GAGCSCATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTGTCTACGSTGTGAATGCAAA 408

Qy        380 TATGAAGAAAGAAGCTCTGTCACAATCAAGGTTACCATTATAATTTATCTCTCCATTTTG 439
              |||||||||||||||||||:|||||||||||||||||||||||||||||||:|||||||
Db        409 TATGAAGAAAGAAGCTCTGTSACAATCAAGGTTACCATTATAATTTATCTCTSCATTTTG 468

Qy        440 GGCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGAGCCCATACTGAAGAGGCGC 499
              |||||||||||||||||||:|||||||||||||||||||||||||||||||||||||||||
Db        469 GGCCTTCTACTTCTGTACATGGTATATSTTACTCTGGTTGAGCCCATACTGAAGAGGCGC 528

Qy        500 CTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATATTGGGGATCACCAGCCTTTT 559
              |||||||||||||||||||||||||||||||||||||||||||||:||||||:||||
Db        529 CTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATATTGGGGATSACCAGCSTTTT 588

Qy        560 GCAAATGCACACGATGTGCTAGCCCGCTCCCGCAGTCGAGCCAACGTGCTGAACAAGGTA 619
              |:|||||||||||||||||||||||||||||:|||||||||||||||||||||||||||||
Db        589 GSAAATGCACACGATGTGCTAGCCCGCTCCCGCAGTSGAGCCAACGTGCTGAACAAGGTA 648

Qy        620 GAATATGCACAGCAGCGCTGGAAGC-TTCAAGTCCAAGAGCAGCGAAAGTCTGTCTTTGA 678
              ||||||||||||||||:|||||| ||||||||||||||||||||||||||||||||||||
Db        649 GAATATGCACAGCAGCGSTGGAAGCGTTCAAGTCCAAGAGCAGCGAAAGTCTGTCTTTGA 708

Qy        679 CCGGCATGTTGTCCTCAGCTAATTGGGAATTGAATTCAAGGTGACTAGAAAGAAACAGGC 738
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        709 CCGGCATGTTGTCCTCAGCTAATTGGGAATTGAATTCAAGGTGACTAGAAAGAAACAGGC 768

Qy        739 AGACAACTGGAAAGAACTGACTGGGTTTTGCTGGGTTTCATTTTAATACCTTGTTGATTT 798
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        769 AGACAACTGGAAAGAACTGACTGGGTTTTGCTGGGTTTCATTTTAATACCTTGTTGATTT 828

Qy        799 CACCAACTGTTGCTGGAAGATTCAAAACTGGAAGCAAAAACTTGCTTGATTTTTTTTTCT 858
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        829 CACCAACTGTTGCTGGAAGATTCAAAACTGGAAGCAAAAACTTGCTTGATTTTTTTTTCT 888

Qy        859 TGTTAACGTAATAATAGAGACATTTTTAAAAGCACACAGCTCAAAGTCAGCCAATAAGTC 918
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        889 TGTTAACGTAATAATAGAGACATTTTTAAAAGCACACAGCTCAAAGTCAGCCAATAAGTC 948

Qy        919 TTTTCCTATTTGTGACTTTTACTAATAAAAATAAATCTGCCTGTAAATTATCTTGAAGTC 978
              ||||||||||||||||||||||||||||||||||:||:|||||||:||||||||||||
Db        949 TTTTCCTATTTGTGACTTTTACTAATAAAAATAAATCKGCSTGTAAATKATCTTGAAGTC 1008

Qy        979 CTTTACCTGGAACAAGCACTCTCTTTTTCACCACATA 1015
              |||||||||| |:||||||||||||||||||||||
Db       1009 CTTTACCTGGGAMAAGCACTCTCTTTTTCACCACATA 1045


RESULT 2
AL575462/c
LOCUS       AL575462               1180 bp    mRNA    linear   EST 01-JUN-2003
DEFINITION  AL575462 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
            clone CS0DI060YL12 3-PRIME, mRNA sequence.
ACCESSION   AL575462
VERSION     AL575462.2  GI:31313770
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1180)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     On Feb 16, 2001 this sequence version replaced gi:12936648.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 6242.f For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0DI060DF06NP1&cluster=6242.f. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0DI060DF06NP1.
FEATURES             Location/Qualifiers
     source          1. .1180
                     /organism="Homo sapiens"
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                     /db_xref="taxon:9606"
                     /clone="CS0DI060YL12"
                     /tissue_type="PLACENTA COT 25-NORMALIZED"
                     /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN

  Query Match             54.3%;  Score 938;  DB 9;  Length 1180;
  Best Local Similarity   94.6%;  Pred. No. 9.7e-168;
  Matches 1004;  Conservative   24;  Mismatches   26;  Indels    7;  Gaps    6;

Qy        630 AGCAGCGCTGGAAGCTTCAAGTCCAAGAGCAGCGAAAGTCTGTCTTTGACCGGCATGTTG 689
              | : : ||  | |:: |||||:|||||||||:|||||||||:|| ||::||||||||||||
Db       1058 ACMGSAGCSTGGARSCTCAAGYCCAAGAGCASCGAAAGTCTKTC-TTRMCCGGCATGTTG 1000

Qy        690 TCCTCAGCTAATTGGGAATTGAATTCAAGGTGACTAGAAAGAAACAGGCAGACAACTGGA 749
              |||||||||||||||:||||| ||| |:||:|||||||||||||||||||||||||||||
Db        999 CCCTCAGCTAATTGGGWATTGATTTC-ADGTKACTAGAAAGAAACAGGCAGACAACTGGA 941

Qy        750 AAGAACTGACTGGGTTTTGCTGGGTTTCATTTTAATACCTTGTTGATTT-CACCAACTGT 808
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Db        940 AAGAACTGACTGGGTTT--GCTGGKTTCATTTTAATACCTTGTTGATTTCCACCAACTGT 883

Qy        809 TGCTGGAAGATTCAAAACTGGAAGCAAAAACTTGCTTGATTTTTTTTTTCTTGTTAACGTA 868

Db        882 TGCTGGAAGATTCAAAACTGGAAGCAAAAACTTGCTTGA-TTTTTTTTCTTGTTAACGTA 824

Qy        869 ATAATAGAGACATTTTTAAAAGCACACAGCTCAAAGTCAGCCAATAAGTCTTTTCCTATT 928

Db        823 ATAATAGAGACATTTTTAAAAGCACACAGCTCAAAGTCAGCCAATAAGTCTTTTCCTATT 764

Qy        929 TGTGACTTTTACTAATAAAAATAAATCTGCCTGTAAATTATCTTGAAGTCCTTTACCTGG 988

Db        763 TGTGACTTTTACTAATAAAAATAAATCTGCCTGTAAATTATCTTGAAGTCCTTTACCTGG 704

Qy        989 AACAAGCACTCTCTTTTTCACCACATAGTTTTAACTTGACTTTCAAGATAATTTTCAGGG 1048

Db        703 AACAAGCACTCTCTTTTTCACCACATAGTTTTAACTTGACTTTCAAGATAATTYCCAGGG 644

Qy       1049 TTTTTGTTGTTGTTGTTTTTTGTTTGTTTGTTTTGGTGGGAGAGGGGAGGGATGCCTGGG 1108

Db        643 TTTTTGTTGTTGTTGTTTTTTGTTTGTTTGTTTTGGTGGGAGAGGGGAGGGATGCCTGGG 584

Qy       1109 AAGTGGTTAACAACTTTTTTCAAGTCACTTTACTAAACAAACTTTTGTAAATAGACCTTA 1168

Db        583 AAGTGGTTAACAACTTTTTTCAAGTCACTTTACTAAACAAACTCTTGTAAATAGACCTTA 524

Qy       1169 CCTTCTATTTTCGAGTTTCATTTATATTTTGCAGTGTAGCCAGCCTCATCAAAGAGCTGA 1228

Db        523 CCTTCTATTTTCGAGTTTCATTTATATTTTGCAGTGTMGCCMGCCTCMTCAAAGCGCTSA 464

Qy       1229 CTTACTCATTTGACTTTTGCACTGACTGTATTATCTGGGTATCTGCTGTGTCTGCACTTC 1288

Db        463 CTCACCCATTTGACTTTTGCACTGACTGTGTTATCTGGGTATCTGCTGTGTCTGCACTTC 404

Qy       1289 ATGGTAAACGGGATCTAAAATGCCTGGTGGCTTTTCACAAAAAGCAGATTTTCTTCATGT 1348

Db        403 ATGGTAAACGGGATCTAAAATGCCTGGTGGCTTTTCACAAAAAGCAGATTTTCTTCATGT 344

Qy       1349 ACTGTGATGTCTGATGCAATGCATCCTAGAACAAACTGGCCATTTGCTAGTTTACTCTAA 1408

Db        343 ACTGTGATGTCTGATGCAATGCATCCTAGAACAAACTGGCCATTTGCTAGTTTACTCTAA 284

Qy       1409 AGACTAAACATAGTCTTGGTGTGTGTGGTCTTACTCATCTTCTAGTACCTTTAAGGACAA 1468

Db        283 AGACTAAACATAGTCTTGGTGTGTGTGGTCTTACTCATCTTCTAGTACCTTTAAGGACAA 224

Qy       1469 ATCCTAAGGACTTGGACACTTGCAATAAAGAAATTTTATTTTAAACCCAAGCCTCCCTGG 1528

Db        223 ATCCTAAGGACTTGGACMCTTGCAATAAAGAAATTTTATTTTAAACCCAAGCCTCCCTGG 164

Qy       1529 ATTGATAATATATACACATTTGTCAGCATTTCCGGTCGTGGTGAGAGGCAGCTGTTTGAG 1588

Db        163 ATTGATAATATATACACATTTGTCAGCATTTCCGGTCGTGGTGAGAGGCAGCTGTTTGAG 104

Qy       1589 CTCCAATATGTGCAGCTTTGAACTAGGGCTGGGGTTGTGGGTGCCTCTTCTGAAAGGTCT 1648

Db        103 CTCCAATGTGTGCAGCTTTGAACTAGGGCTGGGGTTGTGGGTGCCTCTTCTGAAAGGTCT 44

Qy       1649 AACCAT-TATTGGATAACTGGCTTTTTTCTTCCTATGTCCT 1688

Db          43 AACCNTNNNTTGGNTNACTGGCTTTTTTCTTCCBCTTKSSK 3
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RESULT 3
AL537331
LOCUS AL537331 1201 bp mRNA linear EST 31-MAY-2003
DEFINITION AL537331 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone CS0DF025YO05 5-PRIME, mRNA sequence.
ACCESSION AL537331
VERSION AL537331.2 GI:31261954
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1201)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 13, 2001 this sequence version replaced gi:12800824.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 6242.f For more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DF025AH03QP1&cluster=6242.f. Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600 Faraday Avenue Genoscope sequence ID : CS0DF025AH03QP1.
FEATURES Location/Qualifiers
source 1. .1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DF025YO05"
/tissue_type="FETAL BRAIN"
/dev_stage="fetal"
/clone_lib="Homo sapiens FETAL BRAIN"
/note="Organ: brain; Vector: pCMVSPORT_6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."
ORIGIN

Query Match 53.9%; Score 931.2; DB 9; Length 1201;
Best Local Similarity 92.4%; Pred. No. 1.9e-166;
Matches 1051; Conservative 16; Mismatches 54; Indels 17; Gaps 8;

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Qy          3 GCCGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCCGG 62

Db         76 GCCTGAGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCTGAGCCCGAGCCGGGAGCCGG 135

Qy         63 TCGCGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCCAGCGATGGCGACCCTGTGGGGAG 122

Db        136 TCGCGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCCAGCGATGGCGACCCTGTGGGGAG 195

Qy        123 GCCTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTTCCGTGCTGCTGC 182

Db        196 GCCTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTTCCGTGCTGCTGC 255

Qy        183 TGGCGCAGCTGTCAGACGCCGCCAAGAATTTCGAGGATGTCAGATGTAAATGTATCTGCC 242

Db        256 TGGCGCA-STGTCAGACGCCGCCAAGAATTTCGAGGATGTCAGATGTAAATGTATCTGCC 314

Qy        243 CTCCCTATAAAGAAAATTCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTGTG 302

Db        315 CTCCCTATAAAGAAAATTCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTGTG 374

Qy        303 ATTGCCTTCATGTTGTGGAGCCCATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTGTC 362

Db        375 ATTGCCTTCATGTCGTGGAGCCCATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTGTC 434

Qy        363 TACGCTGTGAATGCAAATATGAAGAAAGAAGCTCTGTCACAATCAAGGTTACCATTATAA 422

Db        435 TACGCTGTGAATGCAAATATGAAGAAAGAAGCTCTGTCACAATCAAGGTTACCATTATAA 494

Qy        423 TTTATCTCTCCATTTTGGGCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGAGC 482

Db        495 TTTATCTCTCCATTTTGGGCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGAGC 554

Qy        483 CCATACTGAAGAGGCGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATATTG 542
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Db        555 CCATACTGAAGAGGCGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATATTG 614

Qy        543 GGGATCACCAGCCTTTTGCAAATGCACACGATGTGCTAGCCCGCTCCCGCAGTCGAGCCA 602

Db        615 GGGATCACCAGCCTTTTGCAAATGCACACGATGTGCTAGCCCGCTCCCGCAGTCGAGCCA 674

Qy        603 ACGTGCTGAACAAGGTAGAATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCAGC 662

Db        675 ACGTGCTGAACAAGGTAGAATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCAGC 734

Qy        663 GAAAGTCTGTCTTTGACCGGCATGTTGTCCTCAGCTAATTGGGAATTGAATTCAAGGTGA 722

Db        735 GAAAGTCTGTCTTTGACCGGCATGTTGTCCTCAGCTAATTGGGAATTGAATTCAAGGTGA 794

Qy        723 CTAGAAAGAAACAGGCAGACAACTGGAAAGAACTGACTGGGTTTTGCTGGGTTTCATTTT 782

Db        795 CTAGAAAGAAACAGGCAGACAACTGGAAAGAACTGACTGGGTTTTGCTGGGTTTCATTTT 854

Qy        783 AATACCTTGTTGATTTCACCAACTGTTGCTGGAAGATTCAAAACTGGAAGCAAAAACTTG 842

Db        855 AATACCTTGTTGATTTCACCAACTGTTGCTGGAAGATTCAAAACTGGAAGCAAAAACTTG 914

Qy        843 CTTGA-TTTTTTTTTCTTGTTAACGTAATAATAGAGACATTTTTAAAAGCACACAGCTCA 901

Db        915 CTTGATTTTTTTTTTCTTGTTAACGTAATAATAGAGACATTTTTAAAA-CACACAGCTCA 973

Qy        902 AAGTCAGCCAATAAGTCTTTTCCTATTTGTGACTTTTACTAATAAAAATAAATCTGCCTG 961

Db        974 AAGTCAGCCAATAAGTCTTTTCYTATTTGTGACTTTTACTAAT-AAAAWAAATCTGCCTG 1032

Qy        962 TAAATTATCTTGAAGTCCTTTACCTGGAACAAGCACTCTCTTTTTCACCACATAGTTTTA 1021

Db       1033 TAAATTATYTKG-AGTCCTTTACTKGGACAAGCMYCTCTTTTY----CCACATAGTTTAA 1087

Qy       1022 ACTTGACTTTCAAGATAATTTTCAGGGTTTTTGTTGTTGTTGTTTTTTGTTTGTTTGTTT 1081

Db       1088 MTTGRCTTTCAGA---WAWTTTCAGGGT-----TTGGTGGTGKTGTTTTTTTTKTTGTTT 1139

Qy       1082 TGGTGGGAGAGGGGAGGGATGCCTGGGAAGTGGTTAACAACTTTTTTCAAGTCACTTT 1139

Db       1140 TGTGGGGAGGGGGGGWGCCGGGAAKGGTAAMACTTTTCAAKCAYTTACAAAMAATTTT 1197
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RESULT 4
BX425270

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LOCUS       BX425270               1201 bp    mRNA    linear   EST 15-MAY-2003
DEFINITION  BX425270 Homo sapiens NEUROBLASTOMA Homo sapiens cDNA clone
            CL0BB007ZA11 5-PRIME, mRNA sequence.
ACCESSION   BX425270
VERSION     BX425270.1  GI:30778450
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1201)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 6242.f For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CL0BB007ZA11RP1&cluster=6242.f. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CL0BB007ZA11RP1.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone="CL0BB007ZA11"
                     /tissue_type="NEUROBLASTOMA"
                     /clone_lib="Homo sapiens NEUROBLASTOMA"
                     /note="Vector: pCMVSPORT_6; 1st strand cDNA was primed
                     with a NotI-oligo(dT) primer. Five prime end enriched,
                     double-strand cDNA was digested with Not I and cloned into
                     the Not I and EcoRV sites of the pCMVSPORT 6 vector.
                     Library was not normalized."
ORIGIN
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```
  Query Match             53.9%;  Score 931.2;  DB 13;  Length 1201;
  Best Local Similarity   93.6%;  Pred. No. 1.9e-166;
  Matches 1050;  Conservative   16;  Mismatches   45;  Indels   11;  Gaps    9;

Qy          7 GGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCCGGTCGC 66

Db         37 GGGCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCCGGTCGC 96

Qy         67 GGGGGCTCCGGGCTGTG-GGACCGCTGGGCCCCCAGCGATGGCGACCCTGTGGGGAGGCC 125

Db         97 GGGGGCTCCGGGCTGTGAGGACCGCTGGGCCCCCAGCGATGGCGACCCTGTGGGGAGGCC 156

Qy        126 TTCTTCGGCTTGGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTTCCGTG-CTGCTGCT- 183

Db        157 TTCTTCGGCTTGGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTTCCGTGACTGCTGCTA 216

Qy        184 GGCGCAGCTGTCAGACGCCGCCAAGAATTTCGAGGATGTCAGATGTAAATGTATCTGCCC 243

Db        217 GGCGCASTGGTCAGACGCCGCCAAGAATTTCGAGGATGTCAGATGTAAATGTATCTGCCC 276

Qy        244 TCCCTATAAAGAAAATTCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTGTGA 303

Db        277 TCCCTATAAAGAAAATTCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTGTGA 336

Qy        304 TTGCCTTCATGTTGT-GGAGCCCATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTGTC 362

Db        337 TTGCCTTCATGTTGTAGGAGCCCATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTGTC 396

Qy        363 TACGCTGTGAATGCAAATATGAAGAAAGAAGCTCTGTCACAATCAAGGTTACCATTATAA 422

Db        397 TACGCTGTGAATGCAAATATGAAGAAAGAAGCTCTGTCACAATCAAGGTTACCATTATAA 456

Qy        423 TTTATCTCTCCATTTTGGGCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGAGC 482

Db        457 TTTATCTCTCCATTTTGGGCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGAGC 516

Qy        483 CCATACTGAAGAGGCGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATATTG 542

Db        517 CCATACTGAAGAGGCGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATATTG 576

Qy        543 GGGATCACCAGCCTTTTGCAAATGCACACGATGTGCTAGCCCGCTCCCGCAGTCGAGCCA 602

Db        577 GGGATCACCAGCCTTTTGCAAATGCACACGATGTGCTAGCCCGCTCCCGCAGTCGAGCCA 636

Qy        603 ACGTGCTGAACAAGGTAGAATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCAGC 662

Db        637 ACGTGCTGAACAAGGTAGAATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCAGC 696

Qy        663 GAAAGTCTGTCTTTGACCGGCATGTTGTCCTCAGCTAATTGGGAATTGAATTCAAGGTGA 722

Db        697 GAAAGTCTGTCTTTGACCGGCATGTTGTCCTCAGCTAATTGGGAATTGAATTCAAGGTGA 756

Qy        723 CTAGAAAGAAACAGGCAGACAACTGGAAAGAACTGACTGGGTTTTGCTGGGTTTCATTTT 782

Db        757 CTAGAAAGAAACAGGCAGACAACTGGAAAGAACTGACTGGGTTTTGCTGGGTTTCATTTT 816

Qy        783 AATACCTTGTTGATTTCACCAACTGTTGCTGGAAGATTCAAAACTGGAAGCAAAAACTTG 842

Db        817 AATACCTTGTTGATTTCACCAACTGTTGCTGGAAGATTCAAAACTGGAAGCAAAAACTTG 876
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Qy        843 CTTGATTTTTTTTTCTTGTTAACGTAATAATAGAGACATTTTTAAAAGCACACAGCTCAA 902
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Db        877 CTTGATTTTTTTTTCTTGTTAACGTAATAATAGAGAMATTTTTAAAAGCACACAGCTCAA 936

Qy        903 AGTCAGCCAATAAGTCTTTTCCTATTTGTGACTTTTACTAATAAAAATAAATCTGCCTGT 962
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Db        937 AGTCAGCCAATAAGTCTTTTCCTATTTGTGACTTT--ACTAATAAAAWWAATCTGCCTGT 994

Qy        963 AAATTATCTTGAAGTCCTTTACCTGGAACAAGCACTCTCTTTTTCACCACATAGTTTTAA 1022
              |||||||||||  |:|||||||||||| |:|||||||||||||||||  :     |||||
Db        995 AAATTATCTTG-ARTCCTTTACCTGG-AMAAGCACTCTCTTTTTCACACM--TAGTTTAA 1050

Qy       1023 CTTGACTTTCAAGATAATTTTCAGGGTTTTTGTTGTTGTTGTTTTTTGTTTGTTTGTTTT 1082
              |||||||||| |||:|:|||   || |||:|  |  |:|| |||||||||: ||||
Db       1051 CTTGACTTTC-AGAWAWTTTMAGGGTTTTKTTGTTGTKTTTTTTTTTGTTKTTTTGGCGG 1109

Qy       1083 GGTGGGAGAGGGGAGGGATGCCTGGGAAGTGGTTAACAACTT 1124
              || ||| | | |  |||  |  :   || |  |:|:  |:||
Db       1110 GGAGGGGGGGGTGCYGGGGAGKGKTAAAACTTTTHAWATAMTT 1151
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RESULT 5
AL562476/c
LOCUS AL562476 1201 bp mRNA linear EST 31-MAY-2003
DEFINITION AL562476 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens cDNA clone CS0DC011YH24 3-PRIME, mRNA sequence.
ACCESSION AL562476
VERSION AL562476.2 GI:31286488
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1201)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 15, 2001 this sequence version replaced gi:12910933.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 6173.r
Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation 1600 Faraday Avenue Genoscope sequence ID : CS0DC011DD12NP1.
FEATURES Location/Qualifiers
source 1. .1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DC011YH24"
/tissue_type="NEUROBLASTOMA COT 25-NORMALIZED"
/clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN

Query Match 52.9%; Score 913.8; DB 9; Length 1201;
Best Local Similarity 91.0%; Pred. No. 3.8e-163;
Matches 935; Conservative 33; Mismatches 56; Indels 3; Gaps 2;

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Qy        670 TGTCTTTGACCGGCATGTTGTCCTCAGCTAATTGGGAATTGAATTCAAGGTGACTAGAAA 729
              | | | |   | |:   :||:||||||||||||:||  | |  | |::|||||||||||||
Db       1025 TCTKTCTTGACCGSCATKTGYCCTCAGCTAATKGG--AATTGAATYMAGGTGACTAGAAA 968

Qy        730 GAAACAGGCAGACAACTGGAAAGAACTGACTGGGTTTTGCTGGGTTTCATTTTAATACCT 789
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        967 GAAACAGGCAGACAACTGGAAAGAACTGACTGGGTTTTGCTGGGTTTCATTTTAATACCT 908

Qy        790 TGTTGATTTCACCAACTGTTGCTGGAAGATTCAAAACTGGAAGCAAAAACTTGCTTGATT 849
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 TGTTGATTTCACCAACTGTTGCTGGAAGATTCAAAACTGGAAGCAAAAACTTGCTTGATT 848

Qy        850 TTTTTTTCTTGTTAACGTAATAATAGAGACATTTTTAAAAGCACACAGCTCAAAGTCAGC 909
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Db        847 TTTTTCTCTTGTTAACGTAATAATAGAGACATTTTTAAAAGCACACAGCTCAAAGTCAGC 788

Qy        910 CAATAAGTCTTTTCCTATTTGTGACTTTTACTAATAAAAATAAATCTGCCTGTAAATTAT 969
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Db        787 CAATAAGTCTTTTCCTATTTGTGACTTTTACTAATAAAAATAAATCTGCCTGTAAATTAT 728

Qy        970 CTTGAAGTCCTTTACCTGGAACAAGCACTCTCTTTTTCACCACATAGTTTTAACTTGACT 1029
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Db        727 CTTGAAGTCCTTTACCTGGAACAAGCACTCTCTTTTTCACCACATAGTTTTAACTTGACT 668

Qy       1030 TTCAAGATAATTTTCAGGGTTTTTGTTGTTGTTGTTTTTTGTTTGTTTGTTTTGGTGGGA 1089
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Db        667 TTCAAGATAATTTTCAGGGTTTTTGTTGTTGTTGTTTTTTNGTTTGTTTGTTTTGGNGGGA 608

Qy       1090 GAGGGGAGGGATGCCTGGGAAGTGGTTAACAACTTTTTTCAAGTCACTTTACTAAACAAA 1149
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Qy       1150 CTTTTGTAAATAGACCTTACCTTCTATTTTCGAGTTTCATTTATATTTTGCAGTGTAGCC 1209
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Db        547 CTTTTGTAAATAGACCTTACCTTCTATTTTCGAGTYTCATTTATATTTTGCAGTGTAGCC 488

Qy       1210 AGCCTCATCAAAGAGCTGACTTACTCATTTGACTTTTGCACTGACTGTATTATCTGGGTA 1269
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Db        487 AGCCTCATCAAAGAGCTCACTCACTCATTTSACTTTTGCACTGACTGTATTATCTGGGTA 428

Qy       1270 TCTGCTGTGTCTGCACTTCATGGTAAACGGGATCTAAAATGCCTGGTGGCTTTTCACAAA 1329
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Db        427 TCMGCTGTGTCTGCACTTCATGGTAAACGGGATCYMMAATGCCTGGTGGCTTTTCACAAA 368

Qy       1330 AAGCAGATTTTCTTCATGTACTGTGATGTCTGATGCAATGCATCCTAGAACAAACTGGCC 1389
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Db        367 AAGCASATTTTCTYCATGTACYGTGATGTCTGATGCAATGCATCCTAGAACAMACTGGCC 308

Qy       1390 ATTTGCTAGTTTACTCTAAAGACTAAACATAGTCTTGGTGTGTGTGGTCTTACTCATCTT 1449
              ||||||||||||||||:||:::|||||||||||||||||||||||:|||||||||||||
Db        307 ATTTGCTAGTTTACTCYAAMSMCTAAACATAGTCTTGGTGTGTGTGGSTCTTACTCATCTT 248

Qy       1450 CTAGTACCTTTAAGGACAAATCCTAAGGACTTGGACACTTGCAATAAAGAAATTTTATTT 1509
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Db        247 CTAGTMCCTTTAAGGACAAATCCTAAGCACTTGGACMCYYSCAATAAMSMAATTTTATTT 188

Qy       1510 TAAACCCAAGCCTCCCTGGATTGATAATATATACACATTTGTCAGCATTTCCGGTCGTGG 1569
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Qy       1570 TGAGAGGCAGCTGTTTGAGCTCCAATATGTGCAGCTTTGAACTAGGGCTGGGGTTGTGGG 1629
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Db        127 NNAGACNCACCTNNNNCANCCCCAATNNNNNCANCTNNGAACTAGGGCTGGGGTTGTGGG 68

Qy       1630 TGCCTCTTCTGAAAGGTCTAACCATTATTGGATAAC-TGGCTTTTTTCTTCCTATGTCCT 1688
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Db          67 TGCCTCTTCTGAAAGGTCTAACCATTATTGGATAACNTGCNTTTTTTCTCCCTCTSTCCT 8

Qy       1689 CTTTGGA 1695
              |||||||
Db           7 CTTTGGA 1

RESULT 6
BX440898
LOCUS BX440898 1201 bp mRNA linear EST 15-MAY-2003
DEFINITION BX440898 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone CS0DF012YE14 5-PRIME, mRNA sequence.
ACCESSION BX440898
VERSION BX440898.1 GI:30775890
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KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1201)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 6242.f For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0DF012BC07QP1&cluster=6242.f. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0DF012BC07QP1.
FEATURES             Location/Qualifiers
     source          1. .1201
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DF012YE14"
                     /tissue_type="FETAL BRAIN"
                     /dev_stage="fetal"
                     /clone_lib="Homo sapiens FETAL BRAIN"
                     /note="Organ: brain; Vector: pCMVSPORT_6; 1st strand cDNA
                     was primed with a NotI-oligo(dT) primer. Five prime end
                     enriched, double-strand cDNA was digested with Not I and
                     cloned into the Not I and EcoRV sites of the pCMVSPORT 6
                     vector. Library was not normalized."
ORIGIN

  Query Match             52.3%;  Score 904;  DB 13;  Length 1201;
  Best Local Similarity   93.8%;  Pred. No. 2.7e-161;
  Matches  951;  Conservative   20;  Mismatches   36;  Indels    7;  Gaps    3;

Qy        113 CTGTGGGGAGGCCTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTTCC 172
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Db         61 CTGTGGGGAGGCCTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTTCC 120

Qy        173 GTGCTGCTGCTGGCGCAGCTGTCAGACGCCGCCAAGAATTTCGAGGATGTCAGATGTAAA 232
              |||||||||||||||| :|||||||||||||||||||||||||||||||||||||||||
Db        121 GTGCTGCTGCTGGCGCA-STGTCAGACGCCGCCAAGAATTTCGAGGATGTCAGATGTAAA 179

Qy        233 TGTATCTGCCCTCCCTATAAAGAAAATTCTGGGCATATTTATAATAAGAACATATCTCAG 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 TGTATCTGCCCTCCCTATAAAGAAAATTCTGGGCATATTTATAATAAGAACATATCTCAG 239

Qy        293 AAAGATTGTGATTGCCTTCATGTTGTGGAGCCCATGCCTGTGCGGGGGCCTGATGTAGAA 352
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 AAAGATTGTGATTGCCTTCATGTTGTGGAGCCCATGCCTGTGCGGGGGCCTGATGTAGAA 299

Qy        353 GCATACTGTCTACGCTGTGAATGCAAATATGAAGAAAGAAGCTCTGTCACAATCAAGGTT 412
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Qy        413 ACCATTATAATTTATCTCTCCATTTTGGGCCTTCTACTTCTGTACATGGTATATCTTACT 472
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Db        360 ACCATTATAATTTATCTCTCCATTTTGGGCCTTCTACTTCTGTACATGGTATATCTTACT 419

Qy        473 CTGGTTGAGCCCATACTGAAGAGGCGCCTCTTTGGACATGCACAGTTGATACAGAGTGAT 532
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Db        420 CTGGTTGAGCCCATACTGAAGAGGCGCCTCTTTGGACATGCACAGTTGATACAGAGTGAT 479

Qy        533 GATGATATTGGGGATCACCAGCCTTTTGCAAATGCACACGATGTGCTAGCCCGCTCCCGC 592
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        480 GATGATATTGGGGATCACCAGCCTTTTGCAAATGCACACGATGTGCTAGCCCGCTCCCGC 539

Qy        593 AGTCGAGCCAACGTGCTGAACAAGGTAGAATATGCACAGCAGCGCTGGAAGCTTCAAGTC 652
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Db        540 AGTCGAGCCAACGTGCTGAACAAGGTAGAATATGCACAGCAGCGCTGGAAGCTTCAAGTC 599

Qy        653 CAAGAGCAGCGAAAGTCTGTCTTTGACCGGCATGTTGTCCTCAGCTAATTGGGAATTGAA 712
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Db        600 CAAGAGCAGCGAAAGTCTGTCTTTGACCGGCATGTTGTCCTCAGCTAATTGGGAATTGAA 659

Qy        713 TTCAAGGTGACTAGAAAGAAACAGGCAGACAACTGGAAAGAACTGACTGGGTTTTGCTGG 772
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Db        660 TTCAAGGTGACTAGAAAGAAACAGGCAGACAACTGGAAAGAACTGACTGGGTTTTGCTGG 719

Qy        773 GTTTCATTTTAATACCTTGTTGATTTCACCAACTGTTGCTGGAAGATTCAAAACTGGAAG 832
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Db        720 GTTTCATTTTAATACCTTGTTGATTTCACCAACTGTTGCTGGAAGATTCAAAACTGGAAG 779

Qy        833 CAAAAACTTGCTTGATTTTTTTTTCTTGTTAACGTAATAATAGAGACATTTTTAAAAGCA 892
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Db        780 CAAAAACTTGCTTGATTTTTTTTTCTTGTTAACGTAATAATAGAGACATTTTTAAAAGCA 839

Qy        893 CACAGCTCAAAGTCAGCCAATAAGTCTTTTCCTATTTGTGACTTTTACTAATAAAAATAA 952
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Db        840 CACAGCTCAAAGTCAGCCAATAAGTCTTTTCCTATTTGTGACTTTTACTAATAAAAATAA 899

Qy        953 ATCTGCCTGTAAATTATCTTGAAGTCCTTTACCTGGAACAAGCACTCTCTTTTTCACCAC 1012
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Db        960 ATAGTTTK-ACGTGGGGKCCAAGATAATTTCAGGGGGGGGGGGGGGGGGGGKGGGGGGG 1018

Qy       1073 TGTTTGTTTTGGTGGGAGAGGGGAGGGATGCCTGGGAAGTGGTTAACAACTTTT 1126
              | ||  |      |||: ::::|| :||  ::|::||:|:|||:|: :  |||:
Db       1019 GGGTTTT-----TGGBGSMRRGGGRGGGAKSCYKGGRAGKGGTWAMAMKTTTTY 1067


RESULT 7
AL550557/c
LOCUS       AL550557               1201 bp    mRNA    linear   EST 31-MAY-2003
DEFINITION  AL550557 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
            clone CS0DI058YJ16 3-PRIME, mRNA sequence.
ACCESSION   AL550557
VERSION     AL550557.2  GI:31272374
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1201)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     On Feb 15, 2001 this sequence version replaced gi:12887637.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 6173.r
            Contact : Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0DI058DE08NP1.
FEATURES             Location/Qualifiers
     source          1. .1201
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DI058YJ16"
                     /tissue_type="PLACENTA COT 25-NORMALIZED"
                     /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
```

digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 52.3%; Score 903.4; DB 9; Length 1201;
Best Local Similarity 95.9%; Pred. No. 3.5e-161;
Matches 963; Conservative 7; Mismatches 24; Indels 10; Gaps 4;

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Qy        482 CCCATACTGAAGAGGCGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATATT 541
              :|||||||||||| |||||||||||           :  | | || |::|||||     |
Db       1012 SCCATACTGAAGA-GCGCCTCTTTGACATGCACAKTKATACAGAGTGWKATGAT----AT 958

Qy        542 GGGGATCACCAGCCTTTTGCAAATGCACACGATGTGCTAGCCCGCTCCCGCAGTCGAGCC 601
              |||||||||||||| ||||||||||||||||||||||||||:|||||||||||||||||
Db        957 GGGGATCACCAGCC-TTTGCAAATGCACACGATGTGCTAGCCCSCTCCCGCAGTCGAGCC 899

Qy        602 AACGTGCTGAACAAGGTAGAATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCAG 661
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Db        898 AACGTGCTGAACAAGGTAGAATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCAG 839

Qy        662 CGAAAGTCTGTCTTTGACCGGCATGTTGTCCTCAGCTAATTGGGAATTGAATTCAAGGTG 721
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Db        838 CGAAAGTCTGTCTTTGACCGGCATGTTGTCCTCAGCTAATTGGGAATTGAATTCAAGGTG 779

Qy        722 ACTAGAAAGAAACAGGCAGACAACTGGAAAGAACTGACTGGGTTTTGCTGGGTTTCATTT 781
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Db        778 ACTAGAAAGAAACAGGCAGACAACTGGAAAGAACTRACTGGGTTTTGCTGGGTTTCATTT 719

Qy        782 TAATACCTTGTTGATTTCACCAACTGTTGCTGGAAGATTCAAAACTGGAAGCAAAAACTT 841
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Db        718 TAATACCTTGTTGATTTCACCAACTGTTGCTGGAAGATTCAAAACTGGAAGCAAAAACTT 659

Qy        842 GCTTGATTTTTTTTTCTTGTTAACGTAATAATAGAGACATTTTTAAAAGCACACAGCTCA 901
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Db        658 GCTTGATTTTTTTTTCTTGTTAACGTAATAATAGAGACATTTTTAAAAGCACACAGCTCA 599

Qy        902 AAGTCAGCCAATAAGTCTTTTCCTATTTGTGACTTTTACTAATAAAAATAAATCTGCCTG 961
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Qy        962 TAAATTATCTTGAAGTCCTTTACCTGGAACAAGCACTCTCTTTTTCACCACATAGTTTTA 1021
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Db        538 TAAATTATCTTGAAGTCCTTTACCTGGAACAAGCACTCTCTTTTTCACCACATAGTTTTA 479

Qy       1022 ACTTGACTTTCAAGATAATTTTCAGGGTTTTTGTTGTTGTTGTTTTTTGTTTGTTTGTTT 1081
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Db        478 ACTTGACTTTCAAGATAATTTTCAGGGTTTTTGTTGTTGTTGTTTTTTGTTTGTTTGTTT 419

Qy       1082 TGGTGGGAGAGGGGAGGGATGCCTGGGAAGTGGTTAACAACTTTTTTCAAGTCACTTTAC 1141
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Db        418 TGGTGGGAGAGGGGAGGGATGCCTGGGAAGTGGTTAACAACTTTTTTCAAGTCACTTTAC 359

Qy       1142 TAAACAAACTTTTGTAAATAGACCTTACCTTCTATTTTCGAGTTTCATTTATATTTTGCA 1201
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Db        358 TAAACAAACTTTTGTAAATAGACCTTACCTTCTATTTTCGAGTTTCATTTATATTTTGCA 299

Qy       1202 GTGTAGCCAGCCTCATCAAAGAGCTGACTTACTCATTTGACTTTTGCACTGACTGTATTA 1261
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Db        298 GTGTAGCCAGCCTCATCAAAGAGCTAACTAACTCATTTGACTTTTGCACTGACTGTGTTA 239

Qy       1262 TCTGGGTATCTGCTGTGTCTGCACTTCATGGTAAACGGGATCTAAAATGCCTGGTGGCTT 1321
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Qy       1322 TTCACAAAAAGCAGATTTTCTTCATGTACTGTGATGTCTGATGCAATGCATCCTAGAACA 1381
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Db        178 TTCACAAAAAGCAGATTTTCTTCATGTACTGTGATGTCTGATGCAATGCATCCTAGCACA 119

Qy       1382 ----AACTGGCCATTTGCTAGTTTACTCTAAAGACTAAACATAGTCTTGGTGTGTGTGGT 1437
                  |||||||||||||||||| |||||||||||||||||||||||||||||||||||| |
Db        118 CCACAACTGGCCATTTGCTAGTTAACTCTAAAGACTAAACATAGTCTTGGTGTGTGTGNT 59

Qy       1438 CTTACTCATCTTCTAGTACCTTTAAGGACAAATCCTAAGGACTT 1481
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Db         58 CTAACTCATCTTCTAGTACCTTTAAGGACAAATCCTAAGGAYTT 15
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RESULT 8
AK077253
LOCUS AK077253 1642 bp mRNA linear HTC 18-SEP-2003
DEFINITION Mus musculus 11 days pregnant adult female ovary and uterus cDNA, RIKEN full-length enriched library, clone:5031426I03 product:C11ORF15 PROTEIN homolog [Homo sapiens], full insert sequence.
ACCESSION AK077253
VERSION AK077253.1 GI:26346117
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861
REFERENCE 4
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
REFERENCE 5
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
REFERENCE 6 (bases 1 to 1642)
AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
TITLE Direct Submission
JOURNAL Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC),

```
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.go.jp/
            URL:http://fantom.gsc.riken.go.jp/.
FEATURES             Location/Qualifiers
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                     /db_xref="MGI:2393085"
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Qy         68 GGGGCTCCGGGCTGTGGGACCGCTGGGCCCCCAGCGATGGCGACCCT---GTGGGGAGGC 124
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Db          6 GGGGCTCGGGGCTCGCAGGAGCGGCTGGCTCCCGCGATGGCGAGCCTATGGTGCGGAAAC 65

Qy        125 CTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTTCCGTGCTGCTGCTG 184
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Db         66 CTGCTGCGGCTGGGCTCGGGGCTCAGCATGTCCTGCCTGGCGCTGTCGGTGCTGCTGCTC 125

Qy        185 GCGCAGCTGTCAGACGCCGCCAAGAATTTCGAGGATGTCAGATGTAAATGTATCTGCCCT 244
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Db        126 GCGCAGCTGACAGGCGCCGCCAAGAATTTTGAAGATGTGAGATGTAAATGCATCTGCCCT 185

Qy        245 CCCTATAAAGAAAATTCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTGTGAT 304
              |||||||||| ||| ||||||| |||||||||||||| ||||||||||||||||||||
Db        186 CCCTATAAAGAGAATCCTGGGCACATTTATAATAAGAATATATCTCAGAAAGATTGTGAT 245

Qy        305 TGCCTTCATGTTGTGGAGCCCATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTGTCTA 364
              |||||||||| |||||||||||||||||| ||||| ||||||||||||||||||||||||
Db        246 TGCCTTCATGTCGTGGAGCCCATGCCTGTACGGGGACCTGATGTAGAAGCATACTGTCTA 305

Qy        365 CGCTGTGAATGCAAATATGAAGAAAGAAGCTCTGTCACAATCAAGGTTACCATTATAATT 424
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Db        306 CGCTGTGAATGCAAATACGAAGAGAGAAGCTCTGTCACAATCAAGGTTACCATTATAATT 365

Qy        425 TATCTCTCCATTTTGGGCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGAGCCC 484
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Db        366 TATCTCTCTATTTTGGGCCTTCTGCTTCTGTACATGGTATATCTTACCTTAGTTGAGCCC 425

Qy        485 ATACTGAAGAGGCGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATATTGGG 544
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Db        426 ATCCTGAAGAGGCGCCTCTTTGGACACTCCCAGCTGTTGCAGAGCGATGATGACGTTGGG 485

Qy        545 GATCACCAGCCTTTTGCAAATGCACACGATGTGCTAGCCCGCTCCCGCAGTCGAGCCAAC 604
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Qy        605 GTGCTGAACAAGGTAGAATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCAGCGA 664
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Qy        665 AAGTCTGTCTTTGACCGGCATGTTGTCCTCAGCTAATTGGGAATTGAATTCAAGGTGACT 724
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Db        606 AAGTCTGTCTTCGACCGACACGTTGTCCTCAGCTAACTGGGAACTGGAATC-AGGTGACT 664

Qy        725 AGAAAGAAACAGGCAGACAACTGGAAAGAACTGACTGGGTTTTGCTGGGTTTCATT---T 781
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Db        665 AGGAAG-AACACGCAGACAACTGGGAAGAATTGTCTGGGTGTCCGTGCGTTTTAATGCCA 723

Qy        782 TAATACCTTGTTGATTTCACCAACTGTTGCTGGAAGATTCAAAACTGGAAGCAAAAACTT 841
              | |   || | | ||     | || |||||| || |||||||||| ||||
Db        724 TGTTTGTTTTTACAAATCCTTGCTGGATGGAGGAAGACTCCAAACTGGAAGC--AAACCC 781

Qy        842 GCTTGATTTTTTTTTCTTGTTAACGTAATAATAGAGACATTTTTAAAAGCACACAGCTCA 901
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Db        782 CATGCTTGGTATTTTCCTGTTAATATATTAATAGAGACATTTTTACA-GCACACAGTTCC 840

Qy        902 AAGTCAGCCAATAAGTCTTTTCCTATTTGTGACTTTTACTAATAAAAATAAATCTGCCTG 961
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Db        841 AAGTCAACCAGTAAGTCTTTTCCTACTTGTGACTTTTACTAAT-AAAATTAAGCTGCCTG 899

Qy        962 TAAATTATCTTGAAGTCCTTTACCTGGAACAAGCACTCTCTTTTTCACCACATAGTTTTA 1021
              | | |||||||||||| ||  | |||||||||||| |||||||| |  |||| |||| ||
Db        900 TGAGTTATCTTGAAGCCCCGTGCCTGGAACAAGCTCTCTCTTTCTTGCCACACAGTTCTA 959

Qy       1022 ACTTGACTTTCAAGATAATTTTCAGGGTTTTTGTTGTTGTTGTTTTTTGTTTGTTTGTTT 1081
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Db        960 ACTTGGTGTTCAAGATAACTTCCAGGTGTGTTTTTGCTTCTCTTT--------CTTGTGG 1011

Qy       1082 TGGTGGGAGAGGGGAGGGATGCCTGGGAAGTGGTTAACAACTTTTTTCAAGTCACTTTAC 1141
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Qy       1142 TAAACAAACTTTTGTAAATAGACCTTACCTTCTATTTTCGAGTTTCATTTATATTTTGCA 1201
                | ||| |||| || |||| | ||| |||| || |  | | | || | ||
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Qy       1202 GTGTAGCCAGCCTCATCAAAGAGCTGACTTACTCATTTGACTTTTGCACTGACTGTATTA 1261
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Db       1125 GTGTAG-CTGGCTTGTCAGCGTGCTGGCCTCCCCACTTGACTTTTGCACTGACTACATTA 1183

Qy       1262 TCTGGGTATCTG------CTGTGTCTGCACTTCATGGTAAACGGGATCTAAAATGCCTGG 1315
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Db       1184 CCTAAGATTCTGGTTAGCCTGTGGCTGCATTTCATGACCAGTTGGATCTGAAATGCCTGG 1243

Qy       1316 TGGCTTTTCACAAAAAGCAGATTTTCTTCATGTACTGTGATGTCTGATGCAATGCATCCT 1375
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Qy       1376 AGAACAAACTGGCCATTTGCTAGTTTACTCTAAAGACTAAACATAGTCTTGGTGTGTGTG 1435
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Qy       1436 GTCTTACTCATCTTCTAGTACCTTTAAGGACAAATCCTAAGGACTTGGACACTTGCAATA 1495
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Qy       1496 AAGAAATTTTATTTTAAACCCAAGCCTCCCTGGATTGATAATATATACACATTTGTCAGC 1555
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Qy       1556 ATTTCCGGTCGTGGTGAGAGGCAGCTGTTTGAGCTCCAATATGTGCAGCTTTGAACTAGG 1615
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Db       1532 ACTAGAGTTCTGATTGCCTCTCTCTGAGAAGTCTAACAGTTATTGGATAACTGGCTTTTT 1591

Qy       1675 TCTTCCTATGTCCTCTTTGGAATGTAACAATAAAAATAATTTTTGAAAC 1723
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RESULT 9
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LOCUS       BM924942               1063 bp    mRNA    linear   EST 12-MAR-2002
DEFINITION  AGENCOURT_6627575 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5762204
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ACCESSION   BM924942
VERSION     BM924942.1  GI:19375321
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1063)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM12812  row: a  column: 21
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FEATURES             Location/Qualifiers
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                     spleen, and 20-22 week male spleens.  Library is oligo-dT
                     primed and directionally cloned (EcoRV site is destroyed
                     upon  cloning).  Average insert size 1.4 kb, insert size
                     range 1-3 kb. Library is normalized and enriched for
                     full-length clones and was  constructed by C. Gruber
                     (Invitrogen).  Research Genetics tracking  code 026. Note:
                     this is a NIH_MGC Library."
ORIGIN
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  Best Local Similarity   96.1%;  Pred. No. 2.4e-159;
  Matches 1014;  Conservative    0;  Mismatches   27;  Indels   14;  Gaps    9;

Qy         17 CTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCCGGTCGCGGGGGCTCCG 76
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Qy         77 GGCTGTGGGACCGCTGGGCCCCCAGCGATGGCGACCCTGTGGGGAGGCCTTCTTCGGCTT 136
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Db         69 GGCTGTGGGACCGCTGGGCCCCCAGCGATGGCGACCCTGTGGGGAGGCCTTCTTCGGCTT 128

Qy        137 GGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTTCCGTGCTGCTGCTGGCGCAGCTGTCA 196
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Db        189 GACGCCGCCAAGAAATTTCGAGGATGTCAGATGTAAATGTATCTGCCCTCCCTATAAAGAA 248

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Db        369 AAATATTAAGAAAGAAGCTCTGTCACAATCAAGGTTACCATTATAATTTATCTCTCCATT 428

Qy        437 TTGGGCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGAGCCCATACTGAAGAGG 496
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Db        429 TTGGGCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGAGCCCATACTGAAGAGG 488

Qy        497 CGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATATTGGGGATCACCAGCCT 556
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Qy        557 TTTGCAAATGCACACGATGTGCTAGCCCGCTCCCGCAGTCGAGCCAACGTGCTGAACAAG 616
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Qy        617 GTAGAATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCAGCGAAAGTCTGTCTTT 676
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Qy        677 GACCGGCATGTTGTCCTCAGCTAATTGGGAATTGAATTCAAGGTGACTAGAAAGAAACAG 736
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Qy        737 GCAGACAACTGGAAAGAACTGACTGGG-TTTTGCTGGGTTTCATTTTAATACCTTG-TTG 794
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Db        729 GCAGACAACTGGAAAGAACTGACTGGGTTTTTGCTGGGTTTCATTTTAATACCTTGTTTG 788

Qy        795 ATTTCACCAACTGTTGCTGGAAGATTCAAAACTGGAAGCAAAAACTTGCTTGATTTTTTT 854
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Qy        855 TT--CTTGTTAACGTAATAATAGAGACA-TTTTTAAAAGCACACAGCTCAAAGTCAGCCA 911
              ||  | |||||||| |||||||||||| |||||||||||||||||||  |||||||||
Db        849 TTTCTTGGTTAACGAAATAATAGAGACATTTTTTAAAAGCACACAGCTTCAAGTCAGCCA 908

Qy        912 ATAAGTC--TTTTCCTATTTGTGAC-TTTTACTAATAAAAATAAATCTGCC--TGTAAAT 966
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Db        909 ATAAAGCCTTTTCCCTATTTGTGACTTTTTACTAATAAAAATAAATCTGCCCTGTAAAAT 968

Qy        967 TATCTTGAAGT-CCTTTACCTGGAACAAGCACTCTC---TTTTTCACCACATAGTTTTAA 1022
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Qy       1023 CTTGACTTTCAAGATAATTTTCAGGGTTTTTGTTG 1057
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RESULT 10
AL567498/c

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LOCUS       AL567498               962 bp    mRNA    linear   EST 31-MAY-2003
DEFINITION  AL567498 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
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ACCESSION   AL567498
VERSION     AL567498.2  GI:31290393
KEYWORDS    EST.
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SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 962)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     On Feb 16, 2001 this sequence version replaced gi:12920917.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 6173.r,
            Contact : Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0DF037CB12NP1.
FEATURES             Location/Qualifiers
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                     /clone_lib="Homo sapiens FETAL BRAIN"
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                     was primed with a NotI-oligo(dT) primer. Five prime end
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                     vector. Library was not normalized."
ORIGIN
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Qy        728 AAGAAACAGGCAGACAACTGGAAAGAACTGACTGGGTTTTGCTGGGTTTCATTTTAATAC 787
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Db        962 AARAAAMAKGCAGACAACTGRAAWGAACTTWCTGGGKTTTGCTGKGTTTCATKTTAATAC 903

Qy        788 CTTGTTGATTTCA-CCAACTGTTGCTGGAAGATTCAAAACTGGAAGCAAAAACTTGCTTG 846
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Qy        847 ATTTTTTTTTTCTTGTTAACGTAATAATAGAGACATTTTTAAAAGCACACAGCTCAAAGTC 906
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Db        842 ATTTTTTTTTTCTTGTTAACGTAATAAWAGAGACATTTTTAAAAGYAYACATCTCAAAGTC 783

Qy        907 AGCCAATAAGTCTTTTCCTATTTGTGACTTTTACTAATAAAAATAAATCTGCCTGTAAAT 966
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              ||| |||||| ||| :||||:|||||||||||||||||||||||||||||||||||||||
Db        662 ACTCTCAAGAAAATAYTCAGSGTTTTTGTTGTTGTTGTTTTTTGTTTGTTTGTTTTGGTG 603

Qy       1087 GGAGAGGGGAGGGATGCCTGGGAAGTGGTTAACAACTTTTTTCAAGTCACTTTACTAAAC 1146
              |:|||||||||||||||||||||||||||||||:|||||||||||||||| || ||||
Db        602 GRAGAGGGGAGGGATGCCTGGGAAGTGGTTAACAACKTTTTTCAAGTCACTTAACAAAAC 543

Qy       1147 AAACTTTTGTAAATAGACCTTACCTTCTATTTTCGAGTTTCATTTATATTTTGCAGTGTA 1206
              ||||:||||:|||:|||||||||||||||||||||||| ||||||||||||||||||||
Db        542 AAACKTTTGWAAAWAGACCTTACCTTCTATTTTCGAGTCTCATTTATATTTTGCAGTGTA 483

Qy       1207 GCCAGCCTCATCAAAGAGCTGACTTACTCATTTGACTTTTGCACTGACTGTATTATCTGG 1266
              ||||||||||||||||||:|||||||||||||||||||||||||||||:||||||||||
Db        482 GCCAGCCTCATCAAAGAGCTVACTTACTCATTTGACTTTTGCACTGACTGWATTATCTGG 423
```

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Qy       1267 GTATCTGCTGTGTCTGCACTTCATGGTAAACGGGATCTAAAATGCCTGGTGGCTTTTCAC 1326
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        422 GTATCTGCTGTGTCTGCACCTCATGGTAAACGGGATCTAAAATGCCTGGTGGCTTTTCAC 363

Qy       1327 AAAAAGCAGATTTTCTTCATGTACTGTGATGTCTGATGCAATGCATCCTAGAACAAACTG 1386
              ||||||||||::|| |||||||||||||:|:||:|||||||| ||||||||||||||
Db        362 AAAAAGCAGATYYTCCTCATGTACTGTGATSTCYGAYGCAATGCACCCTAGAACAAACTG 303

Qy       1387 GCCATTTGCTAGTTTACTCTAAAGACTAAACATAGTCTTGGTGTGTGTGGTCTTACTCAT 1446
              ||||||||||||:|||||||||||||||||||||||||||||||:||||||||||
Db        302 CCCATTTGCTAGTTYACTCTAAAGACTAAACATAGTCTTGGTGTGTGTGSTCTTACTCAT 243

Qy       1447 CTTCTAGTACCTTTAAGGACAAATCCTAAGGACTTGGACACTTGCAATAAAGAAATTTTA 1506
              ||||||||||||||||||||||||||||||||||||||||||:||||||||||||||||
Db        242 CTTCTAGTACCTTTAAGGACAAATCCTAAGGACTTGGACACTYGCAATAAAGAAATTTTA 183

Qy       1507 TTTTAAACCCAAGCCTCCCTGGATTGATAATATATACACATTTGTCAGCATTTCCGGTCG 1566
              |:|||||||||||||||||||||||||||||||||||||||||||||||||||||:||
Db        182 TYTTAAACCCAAGCCTCCCTGGATTGATAATATATACACATTTGTCAGCATTTCCGGYCG 123

Qy       1567 TGGTGAGAGGCAGCTGTTTGAGCTCCAATATGTGCAGCTTTGAACTAGGGCTGGGGTTGT 1626
              |||||||||||||||||||||| ||||| |||||||| |||||||||:||||||||||
Db        122 TGGTGAGAGGCAGCTGTTTGAGCCCCAATGTGTGCAGCCTTGAACTAGSGCTGGGGTTGT 63

Qy       1627 GGGTGCCTCTTCTGAAAGGTCTAACCATTATTGGATAACTGGCTTTTTTCTTCCTATGTC 1686
              ||||||: |||||||||||||||||||||||||||||| ||||||||||||||||||||
Db          62 GGGTGCMCCTTCTGAAAGGTCTAACCATTATTGGATAACT-GCTTTTTTCTTCCTATGTC 4

Qy       1687 CTC 1689
              |||
Db           3 CTC 1
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RESULT 11
BX439642
LOCUS       BX439642                1201 bp    mRNA    linear   EST 15-MAY-2003
DEFINITION  BX439642 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE012YN20
            5-PRIME, mRNA sequence.
ACCESSION   BX439642
VERSION     BX439642.1  GI:30789776
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1201)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 6173.r
            Contact : Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0DE012DG10QP1.
FEATURES             Location/Qualifiers
     source          1. .1201
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DE012YN20"
                     /tissue_type="PLACENTA"
                     /clone_lib="Homo sapiens PLACENTA"
                     /note="Vector: pCMVSPORT_6; 1st strand cDNA was primed
                     with a NotI-oligo(dT) primer. Five prime end enriched,
                     double-strand cDNA was digested with Not I and cloned into
                     the Not I and EcoRV sites of the pCMVSPORT 6 vector.
                     Library was not normalized."
ORIGIN
```

```
  Query Match             51.6%;  Score 891.4;  DB 13;  Length 1201;
  Best Local Similarity   99.2%;  Pred. No. 6.7e-159;
  Matches  914;  Conservative    2;  Mismatches    3;  Indels    2;  Gaps    2;

Qy        207 AGAATTTCGAGGATGTCAGATGTAAATGTATCTGCCCTCCCTATAAAGAAAATTCTGGGC 266
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        105 AGAATTTCGAGGATGTCAGATGTAAATGTATCTGCCCTCCCTATAAAGAAAATTCTGGGC 164

Qy        267 ATATTTATAATAAGAACATATCTCAGAAAGATTGTGATTGCCTTCATGTTGTGGAGCCCA 326
              |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        165 ATATTTATAATAAGAACATATCTCAGAAAGATTGTGATTGCCTTCATGTCGTGGAGCCCA 224

Qy        327 TGCCTGTGCGGGGGCCTGATGTAGAAGCATACTGTCTACGCTGTGAATGCAAATATGAAG 386
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        225 TGCCTGTGCGGGGGCCTGATGTAGAAGCATACTGTCTACGCTGTGAATGCAAATATGAAG 284

Qy        387 AAAGAAGCTCTGTCACAATCAAGGTTACCATTATAATTTATCTCTCCATTTTGGGCCTTC 446
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        285 AAAGAAGCTCTGTCACAATCAAGGTTACCATTATAATTTATCTCTCCATTTTGGGCCTTC 344

Qy        447 TACTTCTGTACATGGTATATCTTACTCTGGTTGAGCCCATACTGAAGAGGCGCCTCTTTG 506
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        345 TACTTCTGTACATGGTATATCTTACTCTGGTTGAGCCCATACTGAAGAGGCGCCTCTTTG 404

Qy        507 GACATGCACAGTTGATACAGAGTGATGATGATATTGGGGATCACCAGCCTTTTGCAAATG 566
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        405 GACATGCACAGTTGATACAGAGTGATGATGATATTGGGGATCACCAGCCTTTTGCAAATG 464

Qy        567 CACACGATGTGCTAGCCCGCTCCCGCAGTCGAGCCAACGTGCTGAACAAGGTAGAATATG 626
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        465 CACACGATGTGCTAGCCCGCTCCCGCAGTCGAGCCAACGTGCTGAACAAGGTAGAATATG 524

Qy        627 CACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCAGCGAAAGTCTGTCTTTGACCGGCATG 686
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        525 CACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCAGCGAAAGTCTGTCTTTGACCGGCATG 584

Qy        687 TTGTCCTCAGCTAATTGGGAATTGAATTCAAGGTGACTAGAAAGAAACAGGCAGACAACT 746
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        585 TTGTCCTCAGCTAATTGGGAATTGAATTCAAGGTGACTAGAAAGAAACAGGCAGACAACT 644

Qy        747 GGAAAGAACTGACTGGGTTTTGCTGGGTTTCATTTTAATACCTTGTTGATTTCACCAACT 806
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        645 GGAAAGAACTGACTGGGTTTTGCTGGGTTTCATTTTAATACCTTGTTGATTTCACCAACT 704

Qy        807 GTTGCTGGAAGATTCAAAACTGGAAGCAAAAACTTGCTTGATTTTTTTTTCTTGTTAACG 866
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        705 GTTGCTGGAAGATTCAAAACTGGAAGCAAAAACTTGCTTGATTTTTTTTTCTTGTTAACG 764

Qy        867 TAATAATAGAGACATTTTTAAAAGCACACAGCTCAAAGTCAGCCAATAAGTCTTTTCCTA 926
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        765 TAATAATAGAGACATTTTTAAAAGCACACAGCTCAAAGTCAGCCAATAAGTCTTTTCCTA 824

Qy        927 TTTGTGACTTTTACTAATAAAAATAAATCTGCCTGTAAATTATCTTGAAGTCCTTTACCT 986
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        825 TTTGTGACTTTTACTAATAAAAATAAATCTGCCTGTAAATTATCTTGAAGTCCTTTACCT 884

Qy        987 GGAACAAGCACTCTCTTTTTCACCACATAGTTTTAACTTGACTTTCAAGATAATTTTCAG 1046
              |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        885 GGAACAAGCACTCTCTTTTTCACCACATAGTTTTAACTTGACCTTCAAGATAATTTTCAG 944

Qy       1047 GGTTTTTGTTGTTGTTGTTTTTTGTTTGTTTGTTTTGGTGGGAGAGGGGAGGGATGCCTG 1106
              |||||||||||||||| |||||||||||||||||||||||||||||||||||| |||
Db        945 GGTTTTTGTTGTTGTTG-TTTTTGTTTGTTTGTTTTGGTGGGAGAGGGGAGGGATG-CTG 1002

Qy       1107 GGAAGTGGTTAACAACTTTTT 1127
              |||||||||||:|: |||||
Db       1003 GGAAGTGGTTAAMAMTTTTTT 1023


RESULT 12
AL552487
LOCUS       AL552487               1201 bp    mRNA    linear   EST 31-MAY-2003
DEFINITION  AL552487 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
            clone CS0DI070YH13 5-PRIME, mRNA sequence.
ACCESSION   AL552487
VERSION     AL552487.2  GI:31274302
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1201)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     On Feb 15, 2001 this sequence version replaced gi:12891431.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 6242.f For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0DI070CD07QP1&cluster=6242.f. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0DI070CD07QP1.
FEATURES             Location/Qualifiers
     source          1. .1201
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DI070YH13"
                     /tissue_type="PLACENTA COT 25-NORMALIZED"
                     /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN

  Query Match             51.6%;  Score 890.8;  DB 9;  Length 1201;
  Best Local Similarity   98.5%;  Pred. No. 8.7e-159;
  Matches  936;  Conservative    4;  Mismatches    6;  Indels    4;  Gaps    4;

Qy          1 CAGCCGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         82 CAGCCGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCC 141

Qy         61 GGTCGCGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCCAGCGATGGCGACCCTGTGGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        142 GGTCGCGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCCAGCGATGGCGACCCTGTGGGG 201

Qy        121 AGGCCTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTTCCGTGCTGCT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        202 AGGCCTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTTCCGTGCTGCT 261

Qy        181 GCTGGCGCAGCTGTCAGACGCCGCCAAGAATTTCGAGGATGTCAGATGTAAATGTATCTG 240
              ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        262 GCTGGCGCA-CTGTCAGACGCCGCCAAGAATTTCGAGGATGTCAGATGTAAATGTATCTG 320

Qy        241 CCCTCCCTATAAAGAAAATTCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 CCCTCCCTATAAAGAAAATTCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTG 380

Qy        301 TGATTGCCTTCATGTTGTGGAGCCCATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 TGATTGCCTTCATGTTGTGGAGCCCATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTG 440

Qy        361 TCTACGCTGTGAATGCAAATATGAAGAAAGAAGCTCTGTCACAATCAAGGTTACCATTAT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 TCTACGCTGTGAATGCAAATATGAAGAAAGAAGCTCTGTCACAATCAAGGTTACCATTAT 500

Qy        421 AATTTATCTCTCCATTTTGGGCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGA 480
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Db        501 AATTTATCTCTCCATTTTGGGCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGA 560

Qy        481 GCCCATACTGAAGAGGCGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATAT 540

Db        561 GCCCATACTGAAGAGGCGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATAT 620

Qy        541 TGGGGATCACCAGCCTTTTGCAAATGCACACGATGTGCTAGCCCGCTCCCGCAGTCGAGC 600

Db        621 TGGGGATCACCAGCCTTTTGCAAATGCACACGATGTGCTAGCCCGCTCCCGCAGTCGAGC 680

Qy        601 CAACGTGCTGAACAAGGTAGAATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCA 660

Db        681 CAACGTGCTGAACAAGGTAGAATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCA 740

Qy        661 GCGAAAGTCTGTCTTTGACCGGCATGTTGTCCTCAGCTAATTGGGAATTGAATTCAAGGT 720

Db        741 GCGAAAGTCTGTCTTTGACCGGCATGTTGTCCTCAGCTAATTGGGAATTGAATTCAAGGT 800

Qy        721 GACTAGAAAGAAACAGGCAGACAACTGGAAAGAACTGACTGGGTTTTGCTGGGTTTCATT 780

Db        801 GACTAGAAAGAAACAGGCAGACAACTGGAAAGAACTGACTGGGTTTTGCTGGGTTTCATT 860

Qy        781 TTAATACCTTGTTGATTTCACCAACTGTTGCTGGAAGATTCAAAACTGGAAGCAAAAACT 840

Db        861 TTAATACCTTGTTGATTTCACCAACTGTTGCTGGAAGATTCAAAACTGGAAGCAAAAACT 920

Qy        841 TGCTTGATTTTTTTTTCTTGTTAACGTAATAATAGAGACATTTTTAAAAGCACACAGCTC 900

Db        921 TGCTTGATTTTTTTTTCTTGTTAACGTAATAATAGAGACATTTTTAAAA-SACACAGCTC 979

Qy        901 AAAGTCAGCCAATAAGTCTTTTCCTATTTGTGACTTTTACTAATAAAAAT 950

Db        980 -AARKCAGCCAATAAGTC-TTTCCTATTTGTGACTTTACTATAAAAWAAT 1027
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RESULT 13
AL552032

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LOCUS       AL552032               1190 bp    mRNA    linear   EST 31-MAY-2003
DEFINITION  AL552032 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
            clone CS0DI060YL12 5-PRIME, mRNA sequence.
ACCESSION   AL552032
VERSION     AL552032.2  GI:31273848
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1190)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     On Feb 15, 2001 this sequence version replaced gi:12890542.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 6242.f For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0DI060DF06QP1&cluster=6242.f. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0DI060DF06QP1.
FEATURES             Location/Qualifiers
     source          1. .1190
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DI060YL12"
                     /tissue_type="PLACENTA COT 25-NORMALIZED"
                     /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
```

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  Query Match           51.4%;  Score 888.6;  DB 9;  Length 1190;
  Best Local Similarity  89.7%;  Pred. No. 2.3e-158;
  Matches 1009;  Conservative   23;  Mismatches   72;  Indels   21;  Gaps    7;

Qy         17 CTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCCGGTCGCGGGGGCTCCG 76

Db         54 CTGAGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCCGGTCGCGGGGGCTCCG 113

Qy         77 GGCTGTGGGACCGCTGGGCCCCCAGCGATGGCGACCCTGTGGGGAGGCCTTCTTCGGCTT 136

Db        114 GGCTGTGGGACCGCTGGGCCCCCAGCGATGGCGACCCTGTGGGGAGGCCTTCTTCGGCTT 173

Qy        137 GGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTTCCGTGCTGCTGCTGGCGCAGCTGTCA 196

Db        174 GGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTTCCGTGCTGCTGCTGGCGCA-STGTCA 232

Qy        197 GACGCCGCCAAGAATTTCGAGGATGTCAGATGTAAATGTATCTGCCCTCCCTATAAAGAA 256

Db        233 GACGCCGCCAAGAATTTCGAGGATGTCAGATGTAAATGTATCTGCCCTCCCTATAAAGAA 292

Qy        257 AATTCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTGTGATTGCCTTCATGTT 316

Db        293 AATTCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTGTGATTGCCTTCATGTC 352

Qy        317 GTGGAGCCCATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTGTCTACGCTGTGAATGC 376

Db        353 GTGGAGCCCATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTGTCTACGCTGTGAATGC 412

Qy        377 AAATATGAAGAAAGAAGCTCTGTCACAATCAAGGTTACCATTATAATTTATCTCTCCATT 436

Db        413 AAATATGAAGAAAGAAGCTCTGTCACAATCAAGGTTACCATTATAATTTATCTCTCCATT 472

Qy        437 TTGGGCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGAGCCCATACTGAAGAGG 496

Db        473 TTGGGCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGAGCCCATACTGAAGAGG 532

Qy        497 CGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATATTGGGGATCACCAGCCT 556

Db        533 CGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATATTGGGGATCACCAGCCT 592

Qy        557 TTTGCAAATGCACACGATGTGCTAGCCCGCTCCCGCAGTCGAGCCAACGTGCTGAACAAG 616

Db        593 TTTGCAAATGCACACGATGTGCTAGCCCGCTCCCGCAGTCGAGCCAACGTGCTGAACAAG 652

Qy        617 GTAGAATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCAGCGAAAGTCTGTCTTT 676

Db        653 GTAGAATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCAGCGAAAGTCTGTCTTT 712

Qy        677 GACCGGCATGTTGTCCTCAGCTAATTGGGAATTGAATTCAAGGTGACTAGAAAGAAACAG 736

Db        713 GACCGGCATGTTGTCCTCAGCTAATTGGGAATTGAATTCAAGGTGACTAGAAAGAAACAG 772

Qy        737 GCAGACAACTGGAAAGAACTGACTGGGTTTTGCTGGGTTTCATTTTAATACCTTGTTGAT 796

Db        773 GCAGACAACTGGAAAGAACTGACTGGGTTTTGCTGGGTTTCATTTTAATACCTTGTTGAT 832

Qy        797 TTCACCAACTGTTGCTGGAAGATTCAAAACTGGAAGCAAAAACTTGCTTGATTTTTTTTT 856

Db        833 TTCACCAACTGTTGCTGGAAGATTCAAAACTGGAAGCAAAAMCTTGCTTGATTTTTTTTT 892

Qy        857 CTTGTTAACGTAATAATAGAGACATTTTTAAAAGCACACAGCTCAAAGTCAGCCAATAAG 916

Db        893 CTTGTTAACGTAATAATAGAGACATTTTT-AAAGCACACAGCTCAAAGTCAGCCA--TAA 949

Qy        917 TCTTTTCCTATTTGTGACTTTTACTAATAAAAATAAATCTGCCTGTAAATTATCTTGAAG 976

Db        950 GTCTTTYCTATTTGTGACTTTACTAAWAAAAWAATCTGCTGTAAATAW------CTGGAA 1003
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```
Qy        977 TCCTTTACCTGGAACAAGCACTCTCTTTTTCACCACATAGTTTTAACTTGACTTTCAAGA 1036
              |:||||||||:||  | |||| ||      |||| |   || :  ||||||||:
Db       1004 GTCYTTACCTGGAMCAGCCTCTCTTTT------CACACATAGTTTWACTGACTTTCAR-- 1055

Qy       1037 TAATTTTCAGGGTTTTTGTTGTTG--TTGTTTTTTGTTTGTTTGTTTTGGTGGGAGAGGG 1094
              |: |||||||:||| || ||:||  |||||  ::|||||||  |    || ||     |||
Db       1056 -AWATTTCAGGKTTTGTGGTGKTGTTTTGTTGKKTGTTTGTGGGGRAGGGGGGAGCTGGG 1114

Qy       1095 GAGGGATGCCTGGGAAGTGGTTAACAACTTTTTTCAAGTCACTTT 1139
              : ||    :|    |:|  ||:: ||  ||| | |:: | : ||
Db       1115 ARTGGTAAAMTTTTCARTMTTTMWAAAACTTTGTAAWRCCTMCTT 1159
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RESULT 14
AL576084/c
LOCUS AL576084 1201 bp mRNA linear EST 01-JUN-2003
DEFINITION AL576084 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CS0DI071YI08 3-PRIME, mRNA sequence.
ACCESSION AL576084
VERSION AL576084.2 GI:31314380
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1201)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 16, 2001 this sequence version replaced gi:12937876.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 6173.r
Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation 1600 Faraday Avenue Genoscope sequence ID : CS0DI071BE04NP1.
FEATURES Location/Qualifiers
source 1. .1201
/organism="Homo sapiens"
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/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN

Query Match 51.2%; Score 884; DB 9; Length 1201;
Best Local Similarity 97.9%; Pred. No. 1.7e-157;
Matches 899; Conservative 4; Mismatches 14; Indels 1; Gaps 1;

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Qy        762 GGTTTTGCTGGGTTTCATTTTAATACCTTGTTGATTTCACCAACTGTTGCTGGAAGATTC 821
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Db        928 GGGTTTGGCKGGGTTCATTTTAATACCTTG-TKATTTCACCAACTGTTGCTGGAAGATTC 870

Qy        822 AAAACTGGAAGCAAAAACTTGCTTGATTTTTTTTTCTTGTTAACGTAATAATAGAGACAT 881
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Db        869 AAAACTGGAAGCAAAAACTTGCTTGATTTTTTTTTCTTGTTAACGTAATAATAGAGACAT 810

Qy        882 TTTTAAAAGCACACAGCTCAAAGTCAGCCAATAAGTCTTTTCCTATTTGTGACTTTTACT 941
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Qy        942 AATAAAAATAAATCTGCCTGTAAATTATCTTGAAGTCCTTTACCTGGAACAAGCACTCTC 1001
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Qy       1002 TTTTTCACCACATAGTTTTAACTTGACTTTCAAGATAATTTTCAGGGTTTTTGTTGTTGT 1061
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Qy       1062 TGTTTTTTGTTTGTTTGTTTTGGTGGGAGAGGGGAGGGATGCCTGGGAAGTGGTTAACAA 1121
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Qy       1602 AGCTTTGAACTAGGGCTGGGGTTGTGGGTGCCTCTTCTGAAAGGTCTAACCATTATTGGA 1661
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RESULT 15
AL540345
LOCUS AL540345 953 bp mRNA linear EST 12-MAY-2003
DEFINITION AL540345 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE001YO17 5-PRIME, mRNA sequence.
ACCESSION AL540345
VERSION AL540345.2 GI:30543405
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 953)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 15, 2001 this sequence version replaced gi:12870404.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 6173.r

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          Contact : Feng Liang Email : fliang@lifetech.com URL :
          http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
          Faraday Avenue Genoscope sequence ID : CS0DE001AH09QP1.
FEATURES             Location/Qualifiers
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                     with a NotI-oligo(dT) primer. Five prime end enriched,
                     double-strand cDNA was digested with Not I and cloned into
                     the Not I and EcoRV sites of the pCMVSPORT 6 vector.
                     Library was not normalized."
ORIGIN

  Query Match             50.3%;  Score 869.2;  DB 9;  Length 953;
  Best Local Similarity   98.5%;  Pred. No. 1.1e-154;
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Db        125 GCGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCCAGCGATGGCGACCMTGTGGGGAGGC 184

Qy        125 CTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTTCCGTGCTGCTGCTG 184
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Job time : 4587 secs
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